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OM protein - protein search, using sw model

Run on: August 20, 2005, 11:04:48 ; Search time 161 Seconds
(without alignments)
153.007 Million cell updates/sec

Title: US-09-826-791A-2

Perfect score: 1712

Sequence: 1 MEPNGTFSNNRNCTIENF.....KAKTKCVFVSWLRKETRV 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued P Genes AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1703	69.5	346	US-09-585-876-2	Sequence 2, Appli
2	559	32.7	337	US-09-044-404A-2	Sequence 2, Appli
3	559	32.7	337	US-09-586-924-2	Sequence 2, Appli
4	479	28.0	339	US-08-153-848-44	Sequence 44, Appli
5	479	28.0	339	US-08-812-871-3	Sequence 3, Appli
6	479	28.0	339	US-09-299-843A-44	Sequence 44, Appli
7	479	28.0	339	US-09-088-337B-44	Sequence 44, Appli
8	479	28.0	339	US-09-170-496D-32	Sequence 32, Appli
9	479	28.0	339	US-09-11153-44	Sequence 44, Appli
10	479	28.0	339	PCT-US95-07180-2	Sequence 2, Appli
11	476	27.8	339	US-09-170-496D-182	Sequence 182, Appli
12	461	26.9	362	US-08-513-974B-374	Sequence 374, App
13	445	26.1	373	US-09-745-842-14	Sequence 14, Appli
14	442	25.8	373	US-08-559-524A-4	Sequence 4, Appli
15	442	25.8	373	US-08-749-707-4	Sequence 4, Appli
16	442	25.8	373	US-09-947-922-4	Sequence 4, Appli
17	440	25.7	361	US-08-383-750-4	Sequence 4, Appli
18	440	25.7	361	US-08-352-678-4	Sequence 4, Appli
19	440	25.7	361	US-09-536-954-4	Sequence 4, Appli
20	440	25.7	361	US-09-170-496D-78	Sequence 78, Appli
21	440	25.7	361	US-09-929-583B-4	Sequence 4, Appli
22	440	25.7	361	PCT-US93-09636-4	Sequence 4, Appli
23	439.5	25.6	348	US-08-852-824-17	Sequence 17, Appli
24	439	25.6	302	US-08-467-948A-30	Sequence 30, Appli
25	439	25.6	302	US-08-467-947A-30	Sequence 30, Appli
26	437	25.5	344	US-08-467-948A-8	Sequence 8, Appli
27	437	25.5	344	US-08-467-947A-8	Sequence 8, Appli

28	434	25.4	361	4	US-09-170-496D-206	Sequence 206, App
29	434	25.4	377	4	US-09-745-842-17	Sequence 17, Appli
30	430	25.1	370	3	US-08-781-250-2	Sequence 2, Appli
31	424.5	24.8	374	4	US-09-745-842-15	Sequence 15, Appli
32	419.5	24.5	374	4	US-09-102-710B-3	Sequence 3, Appli
33	416.5	24.3	373	3	US-08-513-974B-373	Sequence 373, App
34	416	24.3	342	3	US-08-988-876-9	Sequence 9, Appli
35	416	24.3	375	1	US-08-442-134A-2	Sequence 2, Appli
36	416	24.3	375	1	US-08-446-088A-2	Sequence 2, Appli
37	416	24.3	375	2	US-08-559-524A-3	Sequence 3, Appli
38	416	24.3	375	3	US-08-749-707-3	Sequence 3, Appli
39	416	24.3	375	4	US-09-947-922-3	Sequence 2, Appli
40	409.5	23.9	342	4	US-09-054-272-2	Sequence 6, Appli
41	406.5	23.7	398	1	US-08-097-938-6	Sequence 6, Appli
42	406.5	23.7	398	1	US-08-476-000-6	Sequence 6, Appli
43	406.5	23.7	398	1	US-08-472-840-6	Sequence 6, Appli
44	406.5	23.7	398	2	US-08-476-976-6	Sequence 6, Appli
45	406.5	23.7	398	2	US-08-476-976-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-585-876-2
; Sequence 2, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
; FILE OF INVENTION: Uses Thereof
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/585,876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/182,061
; EARLIER FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-585-876-2

Query Match		99.5%	Score 1703;	DB 4;	Length 346;
Best Local Similarity		99.4%	Pred No. 3.7e-124;		
Matches 328;		Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MEPNGTFSNNRNCTIENF	KREFFFIVYLIIFFWGLGNGLSIYVFLQPYKSTSVNVF	60	
Db	17	MEPNGTFSNNRNCTIENF	KREFFFIVYLIIFFWGLGNGLSIYVFLQPYKSTSVNVF	76	
Qy	61	MLNLAI	SDLLFIETLPRADYILRGSWIFGDLACRIMSLSLYNMYSSYFLTVLSVR	120	
Db	77	MLNLAI	SDLLFIETLPRADYILRGSWIFGDLACRIMSLSLYNMYSSYFLTVLSVR	136	
Qy	121	FLANVHPRLLHVT	RSRWILCGIITWILIMASSIMLLDSGSEONGSVTSCLENLKYIA	180	
Db	137	FLANVHPRLLHVT	RSRWILCGIITWILIMASSIMLLDSGSEONGSVTSCLENLKYIA	196	
Qy	181	KLQTMNYIALV	VGCLLPFFTLSCYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF	240	
Db	197	KLQTMNYIALV	VGCLLPFFTLSCYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF	256	
Qy	241	FLCFLPYHTLRTV	HTLTKVGLCKDLHKLAVITLALAAANACFNPLLYFAGENFKDRL	300	
Db	257	FLCFLPYHTLRTV	HTLTKVGLCKDLHKLAVITLALAAANACFNPLLYFAGENFKDRL	316	
Qy	301	KSALRKGHP	KOKATKCVFVSWLRKETRV	330	
Db	317	KSALRKGHP	KOKATKCVFVSWLRKETRV	346	

QY	302	SALRK	306
Db	307	STFRK	311
<p>RESULT 3</p> <p>US-09-586-924-2</p> <p>Sequence 2, Application US/09586924</p> <p>Patent No. 6506878</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: SATHE, GANESH M.</p> <p>APPLICANT: HALSEY, WENDY</p> <p>APPLICANT: ELLIS, CATHERINE E.</p> <p>APPLICANT: AMES, ROBERT S.</p> <p>APPLICANT: FOLEY, JAMES J.</p> <p>APPLICANT: SARAU, HENRY M.</p> <p>APPLICANT: CHAMBERS, JON</p> <p>TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL</p> <p>TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR</p> <p>FILE REFERENCE: GH-70001-1D1</p> <p>CURRENT APPLICATION NUMBER: US/09/586,924</p> <p>CURRENT FILING DATE: 2000-06-05</p> <p>PRIOR APPLICATION NUMBER: 09/044,404</p> <p>PRIOR FILING DATE: 1998-03-19</p> <p>PRIOR APPLICATION NUMBER: 08/844,795</p> <p>PRIOR FILING DATE: 1997-04-22</p> <p>NUMBER OF SEQ ID NOS: 2</p> <p>SOFTWARE: FastSeq for Windows Version 3.0</p> <p>SEQ ID NO 2</p> <p>LENGTH: 337</p> <p>TYPE: PRT</p> <p>ORGANISM: HOMO SAPIENS</p> <p>US-09-586-924-2</p>			
<p>Query Match 32.7%; Score 559; DB 4; Length 337;</p> <p>Best Local Similarity 38.0%; Pred. No. 7.7e-36;</p> <p>Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;</p>			
QY	11	NSRNC--TIENFKRFFPIVYLIIFFWGLNGLSIYVFLQPKKSTSVNFMNLALSD	68
Db	10	SSATCHDITDDFRNQVSTLYSMISVVGFGNGFVLYLTKYHKSAFQYMINLAVAD	69
QY	69	LLFISTLPFRADYLRGNSWIFGDLACRIMSYSLYNNMYSSIYFLTVLSVVRFLAMVHPF	128
Db	70	LLCVCTPLRVVYVYVHKGIWLFGLFCLRLSTYALYVNLCSIFFMTAMSFRCIAIVFPV	129
QY	129	RLHVTYSRSAILGIIWI-LIMASSIMLSDSGSEQNGSVTSCLNLYKIAK--LQTM	185
Db	130	QINILVTQKARFVCVGIWIFVILTSSPFLMAKPKQKGNKTKCFEPPQDNQTKNHLVL	189
QY	186	NYIALVWGCLPFFFLTSICYLLIIRVLKVEVPESGLRVSHRKALTITITLIIFFLCFL	245
Db	190	HVSLFVGFIIPFVILVYCYTHIITLTKSKMKN--LSSHKAIGIMVMTAAFLVSFM	247
QY	246	PYHLRTVHLTTW--KVGCLCKD--RLHKALVITLALAAANACFNPLLYFAGENFKDRLK	301
Db	248	PHIORTLHLFHLHNETKPCDSVLRMQKSVVITLSLAASNCDFPLLYFFSGGNFRKL--	306
QY	302	SALRK	306
Db	307	STFRK	311
<p>RESULT 4</p> <p>US-08-153-848-44</p> <p>Sequence 44, Application US/08153848</p> <p>Patent No. 5759804</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Godiska, Ronald</p> <p>APPLICANT: Gray, Patrick W.</p> <p>APPLICANT: Schwaikart, Vicki L.</p>			

; Sequence 44, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-44

Query Match 28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
QY 7 FSNNSRNTCTIEN-FKREFFPIVYLIIFFWGLNGLSIYVFLQPKYKSTSVNFMNLIA 65
DB 15 FSLATAEQCGQTPIENMLFASFYLLDFILALVGNLTALWLFIRDKSGTTPANVFLMHLA 74
QY 66 ISDLFIETLPRADYILRGSNWIFGDLACRIMSYSLYNNMYSSYFLTLVLSVVRFLAMV 125
DB 75 VADLSCLVLPTRLVYHFGSNHWPGEIACRLTGFLFYLNMYASIVFLTCISADRLAIV 134
QY 126 HPFRLHVTISRAMLGIIWILI-MASSIMLLDSGEQNGSVTSCELNLYKIAKLOT 184
DB 135 HPVSKLKRRLPLYAHACAFLLWVAVAMAPLLVSPQTQTNHTVVCLQ--LYR-EKASH 191
QY 185 MNVIALVGCGLPFFTLSTCYLLIIRVLLKVEPESGLRVSHR---KALTITIIITLIIPF 241
DB 192 HALVSLAVAFTEFFITVTTCYLLIIRSL-----RQGLRVEKRLTKAVMTAIVLAIFL 245
QY 242 LCFPLVHTLRTVHLTTWKV--GLCKDRHLKALV--ITLALAAANACFNPLLYFAGENPK 297
DB 246 VCFVPYHNRSVVVLHYRSHGASCATORILANRITSCLTSLINGALDPIMYFFVAEKFR 305

QY 298 DRLKSAL----RKGHPQKAKTK 315
DB 306 HALCNLLCGRLKRGPPSPPEKG 327
RESULT 7
US-09-088-337B-44
; Sequence 44, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-JUN-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44

Query Match 28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
QY 7 FSNNSRNTCTIEN-FKREFFPIVYLIIFFWGLNGLSIYVFLQPKYKSTSVNFMNLIA 65
DB 15 FSLATAEQCGQTPIENMLFASFYLLDFILALVGNLTALWLFIRDKSGTTPANVFLMHLA 74
QY 66 ISDLFIETLPRADYILRGSNWIFGDLACRIMSYSLYNNMYSSYFLTLVLSVVRFLAMV 125
DB 75 VADLSCLVLPTRLVYHFGSNHWPGEIACRLTGFLFYLNMYASIVFLTCISADRLAIV 134
QY 126 HPFRLHVTISRAMLGIIWILI-MASSIMLLDSGEQNGSVTSCELNLYKIAKLOT 184
DB 135 HPVSKLKRRLPLYAHACAFLLWVAVAMAPLLVSPQTQTNHTVVCLQ--LYR-EKASH 191
QY 185 MNVIALVGCGLPFFTLSTCYLLIIRVLLKVEPESGLRVSHR---KALTITIIITLIIPF 241

Db 192 HALVSLAVAFPPFTTTCVLLIIRSL-----RQGLRVBKRLLKTKAVRMIAIVLAIFL 245
Qy 242 LCFPLPYHTLRVTLTTHWKV--GLCKDLRLHKALV--ITLALAAANACFNPLLYFAGENFK 297
Db 246 VCFVPYHVRSVVYLHYRSHGASCATQILALANRITSLTSLNGALDPIIMYFFVAEKR 305
Qy 298 DRLKSAL-----RKGHPOKAKTK 315
Db 306 HALCNLLCGKRLKGPSPSEK 327

RESULT 8
US-09-170-496D-32
; Sequence 32, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: NO. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 32
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-32

Query Match 28.0%; Score 479; DB 4; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

Qy 7 FSNNSNRCTIEN-FKREFFPIVYLIIFFWGVNLGLSIYVFLQPYKKSIVNVFMLNLA 65
Db 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDHKSGETPANVFLMHLA 74
Qy 66 ISDLLFTSTLPPRADYLRGNSNIFGDLACRIMSYSLYNNVSYIYELTVLSVVRELAMV 125
Db 75 VADUSCVLVLPLRLVYHFGSNHWPFGIEACRLTGLFLYNNYASIFLTCISADRFLEAIV 134
Qy 126 HPFRLHVTIRSRAWILCGIWIILI-MASSIMLSDSGSEQNGSVTSCLELNLYKIAKLQT 184
Db 135 HPVSKLRLRPLVLAHLACAFWVAVAMAPLLVSPQTQTNHTVVCLO--LYR-EKASH 191
Qy 185 MNYIALVVGCLLPFTLSICVLLIIRVLLKVEVPESGLRVSHR---KALTTIITLIIFP 241
Db 192 HALVSLAVAFPPFTTTCVLLIIRSL-----RQGLRVBKRLLKTKAVRMIAIVLAIFL 245
Qy 242 LCFPLPYHTLRVTLTTHWKV--GLCKDLRLHKALV--ITLALAAANACFNPLLYFAGENFK 297
Db 246 VCFVPYHVRSVVYLHYRSHGASCATQILALANRITSLTSLNGALDPIIMYFFVAEKR 305
Qy 298 DRLKSAL-----RKGHPOKAKTK 315
Db 306 HALCNLLCGKRLKGPSPSEK 327

RESULT 9
PCT-US93-11153-44
; Sequence 44, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell

; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-44

Query Match 28.0%; Score 479; DB 5; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

Qy 7 FSNNSNRCTIEN-FKREFFPIVYLIIFFWGVNLGLSIYVFLQPYKKSIVNVFMLNLA 65
Db 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDHKSGETPANVFLMHLA 74
Qy 66 ISDLLFTSTLPPRADYLRGNSNIFGDLACRIMSYSLYNNVSYIYELTVLSVVRELAMV 125
Db 75 VADUSCVLVLPLRLVYHFGSNHWPFGIEACRLTGLFLYNNYASIFLTCISADRFLEAIV 134
Qy 126 HPFRLHVTIRSRAWILCGIWIILI-MASSIMLSDSGSEQNGSVTSCLELNLYKIAKLQT 184
Db 135 HPVSKLRLRPLVLAHLACAFWVAVAMAPLLVSPQTQTNHTVVCLO--LYR-EKASH 191
Qy 185 MNYIALVVGCLLPFTLSICVLLIIRVLLKVEVPESGLRVSHR---KALTTIITLIIFP 241
Db 192 HALVSLAVAFPPFTTTCVLLIIRSL-----RQGLRVBKRLLKTKAVRMIAIVLAIFL 245
Qy 242 LCFPLPYHTLRVTLTTHWKV--GLCKDLRLHKALV--ITLALAAANACFNPLLYFAGENFK 297
Db 246 VCFVPYHVRSVVYLHYRSHGASCATQILALANRITSLTSLNGALDPIIMYFFVAEKR 305
Qy 298 DRLKSAL-----RKGHPOKAKTK 315
Db 306 HALCNLLCGKRLKGPSPSEK 327

RESULT 10
PCT-US95-07180-2
; Sequence 2, Application PC/TUS9507180
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: GOCAYNE, JEANINE D
; APPLICANT: RUBEN, STEVEN M
; TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

```
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NJ
; COUNTRY: US
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07180
; FILING DATE: 06-JUNE-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 325800-366
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07180-2

Query Match      28.0%; Score 479; DB 5; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY  7 FSNNSNRNCTIEN-FKREFFPIVYLIIFFGVLGNGLSIYVFLQPYKKSIVNVFVLMNLA 65
Db  15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALWLFIRDHKSGLTPANVFLMHLA 74
QY  66 ISDLLFISTLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLTVLSVVRFLAMV 125
Db  75 VADLSCVLVPTRLVYHFGSNHWPFGIEACRLTGFLFYLNMYASIVFLTCISADRFIAIV 134
QY  126 HPRLHLVTSIRSAILCGIWIILI-MASSIMLLDSGSEONGSVTSCLEINLYKIAKLOT 184
Db  135 HPVKSILKLRPLVYAHACAFWVAVAMAPLVSPQTQVNTHTVVCLQ--LYR-EKASH 191
QY  185 MNVIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIITLIIPF 241
Db  192 HALVSLAVAFPTFTTVCYLLIIRSL-----RQGLRVEKRLTKAVRMIAIVLAIPL 245
QY  242 LCPFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
Db  246 VCFVPYHVNRSVYLVHYRSHGASCATQRIALANRITSCLTSLNGALDPIMYFFVAEKFR 305
QY  298 DRLKSAL----RKGHQPQAKTK 315
Db  306 HALCNLLCGKRLKGPSPPEKG 327

RESULT 11
US-09-170-496D-182
; Sequence 182, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
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; SOFTWARE: Patent in version 3.1
; SEQ ID NO 182
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-182

Query Match      27.8%; Score 476; DB 4; Length 339;
Best Local Similarity 34.8%; Pred. No. 2e-29;
Matches 112; Conservative 61; Mismatches 127; Indels 22; Gaps 9;

QY  7 FSNNSNRNCTIEN-FKREFFPIVYLIIFFGVLGNGLSIYVFLQPYKKSIVNVFVLMNLA 65
Db  15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALWLFIRDHKSGLTPANVFLMHLA 74
QY  66 ISDLLFISTLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLTVLSVVRFLAMV 125
Db  75 VADLSCVLVPTRLVYHFGSNHWPFGIEACRLTGFLFYLNMYASIVFLTCISADRFIAIV 134
QY  126 HPRLHLVTSIRSAILCGIWIILI-MASSIMLLDSGSEONGSVTSCLEINLYKIAKLOT 184
Db  135 HPVKSILKLRPLVYAHACAFWVAVAMAPLVSPQTQVNTHTVVCLQ--LYR-EKASH 191
QY  185 MNVIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIITLIIPF 241
Db  192 HALVSLAVAFPTFTTVCYLLIIRSL-----RQGLRVEKRLTKAVRMIAIVLAIPL 245
QY  242 LCPFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
Db  246 VCFVPYHVNRSVYLVHYRSHGASCATQRIALANRITSCLTSLNGALDPIMYFFVAEKFR 305
QY  298 DRLKSAL----RKGHQPQAKTK 315
Db  306 HALCNLLCGKRLKGPSPPEKG 327

RESULT 12
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ogi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
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; Sequence 14, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-DuBridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Holloper, Gunter
; APPLICANT: Conley, Pamela B.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
; US-09-745-842-14

Query Match      26.1%; Score 446; DB 4; Length 373;
Best Local Similarity 32.1%; Pred. No. 4.5e-27;
Matches 102; Conservative 79; Mismatches 111; Indels 26; Gaps 10;

Qy      6  TFSNNRNC--TIENFKREFFIVILIIFFVGVLGNGLSIYVLPQYKKSIVNVFPLN 63
Db      33  TAAVSFFKALKTGFQFYLPFAVILVFIIGPLGNSVAIWMFVFHMKPMWSGISVYMFN 92

Qy      64  LAISDLLFTSTLPRADYULRGSNWIFGDLACRIMSYSLVNMYSYIFVLTLSVWRFLA 123
Db      93  LAUAEFLYVLTLPALFYFNKTDWIFGDAMCKLQRFIFHNLYGSLFLTCISAHRYSG 152

Qy      124  MVHPFRLHVTIRSAMILGGIIV--ILIMASSIMLDLDSGS--EQNGSVTSCLE-----L 174
Db      153  VVYPLKSLGRKKNAICISVLVWLIIVVAISPILFYSGTGVRKNKIT-CYDTSDEYL 211

Qy      175  NLYKIAKLQTMNVIYALVVGCLLPFTLSICYLIIIRVLLKVEVPESGIRVSHRKALTTII 234
Db      212  RSYFIYSMCT---TVAMFC-VPLVLITLGCYGLIVRALIYKLDLNSPLR---RKSILVI 263

Qy      235  ITLIIFFLCFLPYHTLRTVHLTT----WKVGLC--KDLRHKALVITLALAAANACFNPLL 288
Db      264  IVLTVFAVSYPFHVWKMRLARLDFQTPAMCAFNDRVRVATYQVTRGLASLNSCVDPI 323

Qy      289  YYPAGENFKDLKLSALRK 306
Db      324  YFLAGDTFRRLSRATRK 341

RESULT 14
US-08-559-524A-4
; Sequence 4, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2005, 07:35:07 ; Search time 960 Seconds
(without alignments)
176.027 Million cell updates/sec

Title: US-09-826-791a-2

Perfect score: 1712

Sequence: 1 MEPNGTFSNNRNCTIENF.....KAKTKCFVPSVWLKRETRV 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1712	100.0	346	1 CLT2_HUMAN	Q9ns75 homo sapien
2	1367.5	79.9	345	1 CLT2_PIG	Q95n03 sus scrofa
3	1204	70.3	309	2 Q8R528	Q8r528 mus musculus
4	1197	69.9	309	1 CLT2_MOUSE	Q820a1 mus musculus
5	1187	69.3	309	1 CLT2_RAT	Q824t9 rattus norv
6	567.5	33.1	339	1 CLT1_RAT	Q924t8 rattus norv
7	563	32.9	340	1 CLT1_PIG	Q95n02 sus scrofa
8	560	32.7	352	1 CLT1_MOUSE	Q99ja4 mus musculus
9	559	32.7	337	1 CLT1_HUMAN	Q9y271 homo sapien
10	553	32.3	337	2 Q8IV19	Q8iv19 homo sapien
11	487.5	28.5	337	1 G880_HUMAN	Q96p68 homo sapien
12	479	28.0	337	2 Q6Y1R5	Q6y1r5 rattus norv
13	479	28.0	367	1 G13304_HUMAN	Q13304 homo sapien
14	477	27.9	339	2 Q8N5S7	Q8n5s7 homo sapien
15	477	27.9	347	2 Q7ZZA4	Q7zza4 brachydanio
16	473.5	27.7	349	2 Q6P852	Q6p852 xenopus tro
17	470	27.5	362	1 P2YR_MELGA	P49652 melesgria g
18	468	27.3	337	2 Q6Y1F8	Q6y1f8 mus musculus
19	467	27.3	362	1 P2YR_CHICK	P34996 gallus gall
20	459	26.8	339	2 Q6NS65	Q6ns65 mus musculus
21	457	26.7	357	2 Q3DE05	Q3de05 raja erinac
22	456	26.6	249	2 Q6S9C7	Q6s9c7 chinchilla
23	454	26.5	373	1 P2YR_CAVPO	P59902 cavia porce
24	453	26.5	361	2 Q90X57	Q90x57 xenopus lae
25	449.5	26.3	357	2 Q7TMV7	Q7tmv7 mus musculus
26	447	26.1	308	1 P2Y5_CHICK	P32250 gallus gall
27	447	26.1	373	1 P2YR_RAT	P49651 rattus norv
28	446	26.1	373	1 P2YR_HUMAN	P49000 homo sapien
29	442	25.8	373	1 P2YR_BOVIN	P48042 bos taurus
30	442	25.8	373	1 P2YR_MOUSE	P49650 mus musculus
31	440	25.7	361	1 EB12_HUMAN	P32249 homo sapien

32 439 25.6 373 2 Q8BMJ5 Q8bmj5 mus musculus
33 437 25.5 344 1 P2Y5_HUMAN P2y5 homo sapien
34 437 25.5 344 2 Q7Z3S0 Q7z3s0 homo sapien
35 436.5 25.5 344 1 P2Y5_MOUSE Q8bmc0 mus musculus
36 434 25.4 377 1 P2Y2_HUMAN P41231 homo sapien
37 432 25.2 344 2 Q7Z3S6 Q7z3s6 homo sapien
38 430 25.1 370 1 P2Y9_HUMAN Q99677 homo sapien
39 426 24.9 370 2 Q6NSP5 Q6nsp5 homo sapien
40 425 24.8 370 2 Q8BKK1 Q8bkk1 mus musculus
41 424.5 24.8 374 2 O57466 O57466 melesgria g
42 421.5 24.6 374 1 P2Y2_RAT P41232 rattus norv
43 421 24.6 370 2 Q8BLG2 Q8blg2 mus musculus
44 418.5 24.4 373 1 P2Y2_MOUSE P35383 mus musculus
45 416 24.3 342 1 PAFR_CAVPO P21556 cavia porce

ALIGNMENTS

RESULT 1
CLT2_HUMAN STANDARD; PRT; 346 AA.
AC Q9NS75; Q9HCQ2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DB Cysteinyln leukotriene receptor 2 (CysLTR2) (PSEC0146) (HG57) (HPN321)
DE (NGPCR21).
GN Name=CysLTR2; Synonyms=CysLT2, CysLT2R;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20374466; PubMed=10913337; DOI=10.1006/bbrc.2000.3140;
RA Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,
RA Nishikawa T., Kawai Y., Masuho Y., Isogai T., Suzuki Y., Sugano S.,
RA Furuichi K.;
RT "The molecular characterization and tissue distribution of the human
RT cysteinyln leukotriene CysLT2 receptor.";
RL Biochem. Biophys. Res. Commun. 274:316-322(2000).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=10851239; PubMed=10851239; DOI=10.1074/jbc.M003490200;
RA Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
RA Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
RA Williams D.L., Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
RA Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
RA Lynch K.R., Evans J.F.;
RT "Characterization of the human cysteinyln leukotriene 2 receptor.";
RL J. Biol. Chem. 275:30531-30536(2000).
[3]
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20545741; PubMed=11093801;
RA Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
RA Civelli O.;
RT "Molecular cloning and characterization of a second human cysteinyln
RT leukotriene receptor: discovery of a subtype selective agonist.";
RL Mol. Pharmacol. 58:1601-1608(2000).
[4]
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL FEBS Lett. 520:97-101(2002).
[5]
RN [5]
RP SEQUENCE FROM N.A.
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

[6]
 SEQUENCE FROM N.A.
 PubMed=15057823; DOI=10.1038/nature02379;
 Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,
 Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,
 Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,
 Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,
 Ashwell R.I.S., Babbage A.K., Bagguley C.L., Bailey J., Bannerjee R.,
 Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
 Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
 Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,
 Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
 Deloukas P., Dhami P., Dunham I., Dunn M., Earthrowl M.E.,
 Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,
 Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,
 Grafham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,
 Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
 Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,
 King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,
 Lloyd D.W., Lloyd C., Loveland J.E., Lovell J., Martin S.,
 Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,
 Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
 Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
 Sehra H.K., Showlmore R., Skuce C.D., Smith M., Steward C.A.,
 Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Tubby B.,
 Wall M., Wallis J.M., West A.P., Whitehead S.B., Willey D.B.,
 Wilmang L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
 Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.;
 "The DNA sequence and analysis of human chromosome 13.";
 Nature 428:522-528 (2004).
 [7]
 SEQUENCE OF 17-346 FROM N.A.
 Suga H.;
 "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";
 Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 mediated via a G-protein that activates a phosphatidylinositol-
 calcium second messenger system. Stimulation by BAY u9773, a
 partial agonist, induces specific contractions of pulmonary veins
 and might also have an indirect role in the relaxation of the
 pulmonary vascular endothelium. The rank order of affinities for
 the leukotrienes is LTC4 > LTD4 > LTE4.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
 heart, placenta, spleen, peripheral blood leukocytes and adrenal
 gland. In lung, expressed in the interstitial macrophages, and
 slightly in smooth muscle cells.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB038269; BAB03601.1; -
 DR EMBL; AF254664; AAG17281.1; -
 DR EMBL; AF279611; AAK69485.1; -
 DR EMBL; AB083603; BAB89316.1; -
 DR EMBL; AB083604; AAK93330.1; -
 DR EMBL; AL137118; CAC29102.1; -
 DR EMBL; AB041644; BAB16379.1; -
 DR EMBL; HGNC:18274; CYSLTR2.
 DR MIM; 605666; -
 DR GO; GO:0004974; F-leukotriene receptor activity; NAS.
 DR GO; GO:0006955; P-immune response; NAS.
 DR InterPro; IPR004071; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR01533; CYSLTR2RECPT.
 DR

DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 42 Extracellular (Potential).
 FT TRANSMEM 43 63 1 (Potential).
 FT DOMAIN 64 72 Cytoplasmic (Potential).
 FT TRANSMEM 73 93 2 (Potential).
 FT DOMAIN 94 123 Extracellular (Potential).
 FT TRANSMEM 124 144 3 (Potential).
 FT DOMAIN 145 153 Cytoplasmic (Potential).
 FT TRANSMEM 154 174 4 (Potential).
 FT DOMAIN 175 204 Extracellular (Potential).
 FT TRANSMEM 205 225 5 (Potential).
 FT DOMAIN 226 245 Cytoplasmic (Potential).
 FT TRANSMEM 246 266 6 (Potential).
 FT DOMAIN 267 286 Extracellular (Potential).
 FT TRANSMEM 287 307 7 (Potential).
 FT DOMAIN 308 346 Cytoplasmic (Potential).
 FT DISULFID 111 187 By similarity.
 FT CARBOHYD 20 20 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 30 30 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 181 181 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 346 AA; 39635 MW; EB54AA42DDCESE4 CRC64;
 Query Match 100.0%; Score 1712; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 5.9e-99;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPNGTFSSNNRNCTIENFKREFPIVYLITFFWGLNGLSIYVFLQPKKSTSVNVP 60
 DB 17 MEPNGTFSSNNRNCTIENFKREFPIVYLITFFWGLNGLSIYVFLQPKKSTSVNVP 76
 QY 61 MLNLAISSLFISTLPFRADYYLRGNSMIFGDLACRIMSISLYVNMYSIYFLTVLSVVR 120
 DB 77 MLNLAISSLFISTLPFRADYYLRGNSMIFGDLACRIMSISLYVNMYSIYFLTVLSVVR 136
 QY 121 FLAMVHPRLHVTIRSASWILCGIWIILIMASSIMLDGSEQNGSVTSCLELNLYKIA 180
 DB 137 FLAMVHPRLHVTIRSASWILCGIWIILIMASSIMLDGSEQNGSVTSCLELNLYKIA 196
 QY 181 KLQTNMYIALVVGCLLPPTLSICVYLLIRVLKVEPESGLRVSHRKALTTIITLIIF 240
 DB 197 KLQTNMYIALVVGCLLPPTLSICVYLLIRVLKVEPESGLRVSHRKALTTIITLIIF 256
 QY 241 FLCFLPYHTLRTVHLTTWKVGLCKDLHLKALVITLALAAANACFNPLLYYFAGENFKDL 300
 DB 257 FLCFLPYHTLRTVHLTTWKVGLCKDLHLKALVITLALAAANACFNPLLYYFAGENFKDL 316
 QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
 DB 317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346
 RESULT 2
 CLT2_PIG STANDARD; PRT; 345 AA.
 AC Q95N03;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cysteinyl leukotriene receptor 2 (CYSLTR2).
 GN Name=CYSLTR2; Synonyms=CYSLT2;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
 RA Ohishi T., Soga T., Matsushima H., Furuichi K.;
 RT "Characterization of the cloned rat and porcine cysteinyl leukotriene

Db 317 LKSAALRGRPQ--KTRCGSFVCVWLKKEITRV 345

RESULT 3

Q8R528	PRELIMINARY;	PRT;	309 AA.
ID	Q8R528		
AC	Q8R528;		
DT	01-JUN-2002 (T-EMBLrel. 21, Created)		
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)		
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)		
DE	Cysteinyln leukotriene 2 receptor.		
GN	Names=Cyslstr2;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22013942; PubMed=11854273; DOI=10.1074/jbc.M109447200;		
RA	Ogasawara H., Ishii S., Yokomizo T., Kakinuma T., Komine M.,		
RA	Tamaki K., Shimizu T., Izumi T.;		
RT	"Characterization of Mouse Cysteinyln Leukotriene Receptors mCysLT1 and		
RT	mCysLT2. DIFFERENTIAL PHARMACOLOGICAL PROPERTIES AND TISSUE		
RT	DISTRIBUTION ";		
RL	J. Biol. Chem. 277:18763-18768(2002).		
DR	EMBL; AB058930; BAB86881.1; -.		
DR	MGD; MGI:1917336; Cyslstr2.		
DR	GO; GO:0016021; C:integral to membrane; TAS.		
DR	GO; GO:0001631; F:cysteinyln leukotriene receptor activity; IDA.		
DR	InterPro; IPR004071; Cysleuk receptor.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR01533; CYSLTRRECPTR.		
DR	PRINTS; PR00237; GPCRHHODPSN.		
DR	PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.		
KW	Receptor.		
SQ	SEQUENCE 309 AA; 35226 MW; 96FACCB8AF6974 CRC64;		

Query Match 70.3%; Score 1204; DB 2; Length 309;

Best Local Similarity 73.4%; Pred. NO. 2e-67;

Matches 226; Conservative 30; Mismatches 52; Indels 0; Gaps 0;

Qy	1	MEPNGTFSNNNSNCNIENKREFFPIVLIIFWGLGNGLSIYFLQPKKSTSVNVP	60
Db	1	MEVTGTPSSYSNNRCNIENKREFFPIIYLIIFWGLGNGLSIYFLQPKKSTSVNVP	60
Qy	61	MLNLATSDLLFISTLPRADYILRGSNWIFGDLACRIMSYSLVNMYSYIFELTVLSVVR	120
Db	61	MLNLATSDFLFISTLPRADYIFRGSNWIFGDLACRNMYSYSLVNMYSYIFELTVLSVVR	120
Qy	121	FLAMVHPFRLLHVTYSIRSAWILCGIITWITMASSIMLLDSGSPQSGSVTSCLEINLYKIA	180
Db	121	FLATVHPFRMFHTSVRSAWILCGIITWVTFMASSALLVNGQEKNIISCLELSQPKPK	180
Qy	181	KLQTMNYIALVQCLLPFFTLSCYLLIIRVLKVEPSSGLRVSHRKALTITIIILIF	240
Db	181	SLLIIMNHIAVAGFLLPFLTLTCYLLIIRILLKASIPSGPPRAHRKALTITIVIAMITF	240
Qy	241	FLCFLPHTLTVHLTTWKVGLCKDLHKALVITLALAAANACFNPLLYYFAGENFKRL	300
Db	241	LLCFLPYHALRTLUHLVTWDKDSGDLVHKATVITLTMAAANSCFNPLLYYFAGENFKARL	300
Qy	301	KSALRKGH 308	
Db	301	RAIFSKVH 308	

RESULT 4

CLT2_MOUSE	STANDARD;	PRT;	309 AA.
ID	CLT2_MOUSE		
AC	Q20A1;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		


```
FT TRANSMEM 138 158 4 (Potential).
FT DOMAIN 159 187 Extracellular (Potential).
FT TRANSMEM 188 208 5 (Potential).
FT DOMAIN 209 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT DOMAIN 251 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT DOMAIN 293 309 Cytoplasmic (Potential).
FT DISULFID 95 171 By similarity.
FT CARBOHYD 14 14 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 166 166 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 167 167 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 309 AA; 35507 MW; A122AC8177879D56 CRC64;

Query Match 69.3%; Score 1187; DB 1; Length 309;
Best Local Similarity 73.1%; Pred. No. 2.3e-66;
Matches 225; Conservative 26; Mismatches 57; Indels 0; Gaps 0;

QY 1 MEPNGTSSNNRNCTIENFKREFPIVYLIIFWGLVGNGLSIYVFLQPKKSTSVNVF 60
DB 1 MGVGTGTPSYSDKNCTIENFKREFPIYIYLIIFWGLVGNGLSIYVFLQPKKSTSVNVF 60

QY 61 MLNLAISDLFIETLPRADYLRGSGNIWFGDLACRIMSYSLYNNMYSSYFLTVLSVR 120
DB 61 MLNLAISDLFIETLPRADYLRGSGNIWFGDLACRIMSYSLYNNMYSSYFLTVLSVR 120

QY 121 FLAMVHPFRLHVTIRSAILCGIWIILIMASSIMLLDGSQNGSVTSCLELNLYKIA 180
DB 121 FLAMVHPFRLHVTIRSAILCGIWIILIMASSIMLLDGSQNGSVTSCLELNLYKIA 180

QY 121 FLATAPFQMLHITSVSAMILGIIWFWIMASSGLLLKKGKNTTICFELNLQKFK 180
DB 121 FLATAPFQMLHITSVSAMILGIIWFWIMASSGLLLKKGKNTTICFELNLQKFK 180

QY 181 KLQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEPESGLRVSHRKALTTIITLIIF 240
DB 181 KLQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEPESGLRVSHRKALTTIITLIIF 240

QY 181 NLVLINLVALGVGLLPFTLTICYLLIIRVLKVEIPESGPRDAQRKALTTIVAMII 240
DB 181 NLVLINLVALGVGLLPFTLTICYLLIIRVLKVEIPESGPRDAQRKALTTIVAMII 240

QY 241 FLCPLPHTLTHTVLTWVKGLCKDRHLKALVITLALAAANACNPLLYYPAGENFKDL 300
DB 241 FLCPLPHTLTHTVLTWVKGLCKDRHLKALVITLALAAANACNPLLYYPAGENFKDL 300

QY 301 KSLARKGH 308
DB 301 RAIFSKDH 308
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RESULT 6
CLTI_RAT ID CLTI_RAT STANDARD; PRT; 339 AA.
AC Q224T8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyl leukotriene receptor 1 (CysLTR1).
GN Name=CysLTR1; Synonyms=CysLTR;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
RA Ohishi T., Soga T., Matsushime H., Furuichi K.;
RT "Characterization of cloned rat and porcine cysteinyl leukotriene
RT receptors."
RL Submitted (DDBJ/EMBL/GenBank) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating
CC constriction of the microvascular smooth muscle during an
CC inflammatory response. This response is mediated via a G-protein
CC that activates a phosphatidylinositol-calcium second messenger
CC system [By similarity].
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL database
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB052685; BAB60825.1; -.
DR GGD; 619796; CysLTR1.
DR InterPro; IPR004071; Cysleuk receptor.
DR InterPro; IPR000276; GPCR_Rhodpan.
DR Pfam; PF00001; 7tm_1; 1.1.cpftr.
DR PRINTS; PRO1533; CYSLTRCPTTR.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; FALSE_NEG.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 51 1 (Potential).
FT DOMAIN 52 59 Cytoplasmic (Potential).
FT TRANSMEM 60 80 2 (Potential).
FT DOMAIN 81 108 Extracellular (Potential).
FT TRANSMEM 109 129 3 (Potential).
FT DOMAIN 130 143 Cytoplasmic (Potential).
FT TRANSMEM 144 164 4 (Potential).
FT DOMAIN 165 195 Extracellular (Potential).
FT TRANSMEM 196 216 5 (Potential).
FT DOMAIN 217 232 Cytoplasmic (Potential).
FT TRANSMEM 233 253 6 (Potential).
FT TRANSMEM 254 278 Extracellular (Potential).
FT TRANSMEM 279 299 7 (Potential).
FT DOMAIN 300 339 Cytoplasmic (Potential).
FT DISULFID 98 175 By similarity.
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 339 AA; 39143 MW; 281B41DF050DF8EA CRC64;

Query Match 33.1%; Score 567.5; DB 1; Length 339;
Best Local Similarity 36.7%; Pred. No. 7.8e-28;
Matches 122; Conservative 70; Mismatches 115; Indels 25; Gaps 8;

QY 6 TFSNNRNCTIENFKREFPIVYLIIFWGLVGNGLSIYVFLQPKKSTSVNVFMINLA 65
DB 10 TFSNNRNCTIENFKREFPIVYLIIFWGLVGNGLSIYVFLQPKKSTSVNVFMINLA 65

QY 66 ISDLFIETLPRADYLRGSGNIWFGDLACRIMSYSLYNNMYSSYFLTVLSVVRFLAMV 125
DB 66 ISDLFIETLPRADYLRGSGNIWFGDLACRIMSYSLYNNMYSSYFLTVLSVVRFLAMV 125

QY 69 IADLLCVLTPLRVVYVHKWFGDFCLRTLYALYNNLYCSIFPMTAMSPRCVAIV 128
DB 69 IADLLCVLTPLRVVYVHKWFGDFCLRTLYALYNNLYCSIFPMTAMSPRCVAIV 128

QY 126 HPPRLHVTIRSAILCGIWI-LIMASSIMLLDGSQNGSVTSCLELNLYKIAK--L 182
DB 126 HPPRLHVTIRSAILCGIWI-LIMASSIMLLDGSQNGSVTSCLELNLYKIAK--L 182

QY 129 FPVQINLVTKKARFVCVGIMFVILTSPPFLSKSYQDEKNTKCFEPQDKTKKYV 188
DB 129 FPVQINLVTKKARFVCVGIMFVILTSPPFLSKSYQDEKNTKCFEPQDKTKKYV 188

QY 183 QTMNYIALVVGCLLPFTLSICYLLIIRVLKVEPESGLRVSHRKALTTIITLIIFFL 242
DB 183 QTMNYIALVVGCLLPFTLSICYLLIIRVLKVEPESGLRVSHRKALTTIITLIIFFL 242

QY 189 LVLYHVSILFGFIPIFPIVTCYMTILTLKNTMKKN--LPSSRRKAIIGMIIVTAAFLV 246
DB 189 LVLYHVSILFGFIPIFPIVTCYMTILTLKNTMKKN--LPSSRRKAIIGMIIVTAAFLV 246

QY 243 CFLPYHTLRTVHL--TWKVLCKD--RLHKALVITLALAAANACNPLLYYPAGENFKD 298
DB 243 CFLPYHTLRTVHL--TWKVLCKD--RLHKALVITLALAAANACNPLLYYPAGENFKD 298

QY 247 SFNPHYQRAHLHLFLHSETRSCDSVLRMQKSVVITLSLAASNCDFPLLYFFSGGNFR 306
DB 247 SFNPHYQRAHLHLFLHSETRSCDSVLRMQKSVVITLSLAASNCDFPLLYFFSGGNFR 306

QY 299 RLKSLARK-----GHPQKATKC 316
DB 299 RLKSLARK-----GHPQKATKC 316

QY 307 RL-STFKHSLSSMTVIPKKKASLPKGBEMC 337
DB 307 RL-STFKHSLSSMTVIPKKKASLPKGBEMC 337

RESULT 7
CLTI_PIG ID CLTI_PIG STANDARD; PRT; 340 AA.
AC Q95N02;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyl leukotriene receptor 1 (CysLTR1).
```



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FT DISULFID 106 183 By similarity.
FT CARBOHYD 10 10 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 23 23 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 176 176 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 179 179 N-linked (GlcNAc... ) (Potential).
FT CONFLICT 14 14 F -> L (in Ref. 5).
FT CONFLICT 236 236 K -> R (in Ref. 5).
FT SEQUENCE 337 AA; 6814EA0044756CE6 CRC64;

Query Match 28.5%; Score 487.5; DB 1; Length 337;
Best Local Similarity 34.9%; Pred. No. 7.3e-23;
Matches 111; Conservative 64; Mismatches 114; Indels 29; Gaps 10;

QY 14 NCTIEN--FKREFPPIVYLIIFFWVLGNG--LSIYVF-LQPKKSTSVNFMNLAIKD 68
Db 23 NCTDENIPLKMHVLPVIYGIIFVPGNAVISTYIFKMRPKSST---IIMNLACTD 79

QY 69 LLFISTLPFRADYYLGRNSWIFGDLACRIMSYSLVNMYSYIYFLTVLSVVRFLAMVHPF 128
Db 80 LLYLTSPLFIHYASGENWIFGDFMCKFRFSFHNLYSSILFLTCFSLFRVVIHHPM 139

QY 129 RLHVTSIRSAWILCGIHWILIMASSI---MLLDSGSEONGSVTSCLEL-NYKIAKLOT 184
Db 140 SCFSIHKTRCAVAVACAVWVIISLVAVIPMTFLTITSTNRTNRSACLDLTSSDELNTIK--- 196

QY 182 LQTMVIALVVGCLLPFFTLISICYLIIIRVLKVEPESGLRVSHRKALTTIITLIIFP 241
Db 197 --WYNILTATTTCPLPLVITCYTIIHTLTHGLQDSCLK--QKARRLTILLLAFY 251

QY 242 LCFPLVHTLTVHLLTWKVL---CKDRLHKALVITLALAAANACFNPLLYYFAGNFKD 298
Db 252 VCFPLPHILVRIRIESRLSISCSIEHQHEAVIVSRPLAALNTFGNLLYVVVSDNFQ 311

QY 299 RLKSALR---KGHPQAK 313
Db 312 AVCSTVRCKVSGNLEQAK 329

RESULT 12
Q6Y1R5
ID Q6Y1R5 PRELIMINARY; PRT; 337 AA.
AC Q6Y1R5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE G protein-coupled receptor 80.
GN Names=Gpr80;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15001573; DOI=10.1074/jbc.M400360200;
RA Imbe H., Watanabe S., Miyawaki M., Tanabe E., Encinas J.A.;
RT "Identification and Characterization of a Cell-Surface Receptor,
RT P2Y15, for AMP and Adenosine.";
RL J. Biol. Chem. 279:19790-19799(2004).
DR EMBL; AV191367; AAP32736.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR InterPro; IPR002286; P2_purinocptor.
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PRO0237; GPCRHOOPS.
DR PRINTS; PRO1157; P2PURNOCPTR.
DR PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.
KW Receptor.
SQ SEQUENCE 337 AA; 38377 MW; 98995E80DE0531CB9 CRC64;
```

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CC EMBL; U33447; AAB16746.1; -.
CC EMBL; Y12546; CAA73144.1; -.
CC EMBL; Z94154; CAB08107.1; -.
CC EMBL; Z94155; CAB08108.1; -.
CC HSSP; P34996; 1DDO.
CC Genew; HGNC:4471; GPR17.
CC H-invDB; HIX0002439; -.
CC MIM; 603071; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004950; F:chemokine receptor activity; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC InterPro; IPR002286; P2_purinoceptor.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein; Transmembrane.
KW DOMAIN 1 64 Extracellular (Potential).
FT TRANSMEM 65 85 1 (Potential).
FT DOMAIN 86 92 Cytoplasmic (Potential).
FT TRANSMEM 93 113 2 (Potential).
FT DOMAIN 114 133 Extracellular (Potential).
FT TRANSMEM 134 154 3 (Potential).
FT DOMAIN 155 175 Cytoplasmic (Potential).
FT TRANSMEM 176 196 4 (Potential).
FT DOMAIN 197 223 Extracellular (Potential).
FT TRANSMEM 224 244 5 (Potential).
FT DOMAIN 245 260 Cytoplasmic (Potential).
FT TRANSMEM 261 281 6 (Potential).
FT DOMAIN 282 308 Extracellular (Potential).
FT TRANSMEM 309 329 7 (Potential).
FT DOMAIN 330 367 Cytoplasmic (Potential).
FT DISULFID 132 209 By similarity.
FT CARBOHYD 42 42 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 204 204 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 282 282 N-linked (GlcNAc. . .) (Potential).
FT VARSPLIC 1 28 Missing (in isoform 2).
FT /FTID=VSP_001987.
SQ SEQUENCE 367 AA; 40989 MW; 132FBE97BE83C60C CRC64;
Query Match 28.0%; Score 479; DB 1; Length 367;
Best Local Similarity 34.8%; Pred. No. 2.6e-22;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
QY 7 FSNNSNRCNTIEN-FKREFFPIVYLIIFFWGLNGLSIYVLPQYKKSIVNVFMLNLA 65
DB 43 FSLATAEQCQOEFTPLENMFASFYLLDFILALVNTLALWFFIRDKHSGTPANVFLMHLA 102
QY 66 ISDLFLFTSLPFRADYYLRGNSWIFGDLACRINSYSLYVNMYSIYPLTIVLSVVRFLAMV 125
DB 103 VADLSCVLVLPTRLVYHFSGNHPFGEIACRLGFLFLYLNWYASIVFLTICISADRFIAIV 162
QY 126 HPFRLLHVTIRSRAWILCGIWIILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLOT 184
DB 163 HPVKSLLRRPLVLAHLACAFWVAVAMAPLLVSPQVTQNTHTVVCLOQ--LYR-EKASH 219
QY 185 MNVIALVVGCLLPFTLSICVLIILVLLKVEPESGLRVSHR---KALTTIITLIIF 241
DB 220 HALVLSAVATFPFTTTCVLLIIRSL-----RQGLRVEKRLUKTKAVRMIAIVLAIFL 273
QY 242 LCFPYHTLRVTLVLTWKV--GLCKDRHLKALV--ITLAAANACPNFLLYFAGENFK 297
DB 274 VCFPYHVNRSVYVLYHRSHGASCATORILANRITSLTSLNGALDPIYFVAEKFR 333
QY 298 DRKLSAL-----RKGHPOKATK 315
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Db 334 HALCNLLGKRLKGLPPPPSPFEGK 355
RESULT 14
Q8N5S7 PRELIMINARY; PRT; 339 AA.
ID Q8N5S7
AC Q8N5S7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GPR17 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031653; AAB31653.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR002276; GPCR_Rhodopsn.
DR InterPro; IPR002286; P2_purinoceptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR01157; P2YPURNOCPTR.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; UNKNOWN_1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
SQ SEQUENCE 339 AA; 37860 MW; BB0CAFDF0FC371D63 CRC64;
Query Match 27.9%; Score 477; DB 2; Length 339;
Best Local Similarity 34.8%; Pred. No. 3.3e-22;
Matches 112; Conservative 61; Mismatches 127; Indels 22; Gaps 9;
QY 7 FSNNSNRCNTIEN-FKREFFPIVYLIIFFWGLNGLSIYVLPQYKKSIVNVFMLNLA 65
DB 15 FSLATAEQCQOEFTPLENMFASFYLLDFILALVNTLALWFFIRDKHSGTPANVFLMHLA 74
QY 66 ISDLFLFTSLPFRADYYLRGNSWIFGDLACRINSYSLYVNMYSIYPLTIVLSVVRFLAMV 125
DB 75 VADLSCVLVLPTRLVYHFSGNHPFGEIACRLGFLFLYLNWYASIVFLTICISADRFIAIV 134
QY 126 HPFRLLHVTIRSRAWILCGIWIILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLOT 184
DB 135 HPVKSLLRRPLVLAHLACAFWVAVAMAPLLVSPQVTQNTHTVVCLOQ--LYR-EKASH 191
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2005, 04:45:55 ; Search time 213 Seconds
(without alignments)
7628.276 Million cell updates/sec

Title: US-09-826-791A-1

Perfect score: 993

Sequence: 1 atggaacaaatggcactt.....gaaagaaacaagagtataa 993

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patent NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	989.8	99.7	1401	US-09-585-876-1	Sequence 1, Appli
2	145.2	14.6	1578	US-09-044-404A-1	Sequence 1, Appli
3	145.2	14.6	1578	US-09-586-924-1	Sequence 1, Appli
4	99.4	10.0	1020	US-09-170-496D-31	Sequence 31, Appl
5	99.4	10.0	1900	US-09-016-434-1484	Sequence 1484, Ap
6	99.4	10.0	1901	US-08-153-848-43	Sequence 43, Appl
7	99.4	10.0	1901	US-09-299-843A-43	Sequence 43, Appl
8	99.4	10.0	1901	US-09-088-337B-43	Sequence 43, Appl
9	99.4	10.0	1901	5 PCT-US93-11153-43	Sequence 43, Appl
10	99.4	10.0	2453	US-09-07180-1	Sequence 181, App
11	96.2	9.7	1020	US-09-170-496D-181	Sequence 3, Appli
12	92	9.3	1255	US-08-097-938-3	Sequence 3, Appli
13	92	9.3	1255	US-08-476-000-3	Sequence 3, Appli
14	92	9.3	1255	US-08-472-840-3	Sequence 3, Appli
15	92	9.3	1255	US-08-476-976-3	Sequence 3, Appli
16	92	9.3	1255	US-08-474-410-3	Sequence 3, Appli
17	92	9.3	1255	US-08-486-673B-3	Sequence 3, Appli
18	90	9.1	1224	US-08-742-400A-1	Sequence 1, Appli
19	90	9.1	1414	US-08-476-000-62	Sequence 62, Appl
20	90	9.1	1414	US-08-472-840-62	Sequence 62, Appl
21	90	9.1	1414	US-08-476-976-62	Sequence 62, Appl
22	90	9.1	1414	US-08-474-410-62	Sequence 62, Appl
23	90	9.1	1414	US-08-486-673B-62	Sequence 62, Appl
24	85.6	8.6	1567	US-08-889-108-16	Sequence 16, Appl
25	85.6	8.6	1567	5 PCT-US94-10358-16	Sequence 16, Appl
26	85.6	8.6	2706	US-08-454-549-1	Sequence 1, Appli
27	85.6	8.6	2706	US-08-454-552-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-585-876-1
; Sequence 1, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/585,876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/182,061
; EARLIER FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)...(1237)
US-09-585-876-1

Query Match		99.7%	Score 989.8;	DB 4;	Length 1401;
Best Local Similarity		99.8%	Pred. NO. 8.2e-307;		
Matches 991;		Conservative	0;	Mismatches	2;
				Indels	0;
				Gaps	0;
Qy	1	ATCGAACCAATGGCACCCTTCAGCAATACAAACAGCAGGAACTGCACAAATTTGAAACCTC	60		
Db	245	ATGGAACCAATGGCACCCTTCAGCAATACAAACAGCAGGAACTGCACAAATTTGAAACCTC	304		
Qy	61	AAGAGAGAATTTTCCCAATTTGATATCTGATAATATTTTCTGGGAGCTTTGGGAAAT	120		
Db	305	AAGAGAGAATTTTCCCAATTTGATATCTGATAATATTTTCTGGGAGCTTTGGGAAAT	364		
Qy	121	GGTTGTCCATATATGTTTTCCTGAGCCTTATAAGAGTCCACATCTGTGAACGTTTC	180		
Db	365	GGTTGTCCATATATGTTTTCCTGAGCCTTATAAGAGTCCACATCTGTGAACGTTTC	424		
Qy	181	ATGCTAAATCTGGCCATTTCCAGATCTCTGTTCCATAGCACGCTTCCCTTCAGGGCTGAC	240		
Db	425	ATGCTAAATCTGGCCATTTCCAGATCTCTGTTCCATAGCACGCTTCCCTTCAGGGCTGAC	484		
Qy	241	TATTATCTTAGAGGCTCCCAATTTGGATATTTGGAGACCTGCGCTGCAGGATTATGCTTAT	300		
Db	485	TATTATCTTAGAGGCTCCCAATTTGGATATTTGGAGACCTGCGCTGCAGGATTATGCTTAT	544		
Qy	301	TCCTTGTATGTCAAATGTATACAGCATATTTATTTCTCTGACCGTGTGAGTGTGTGCGGT	360		

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Db 545 TCCTTGATGCAACATGACAGAGTAATTAATTCCTGACCGTCTGAGTGTGTGGCT 604
Qy 361 TTCTTGGCAATGTTACCCCTTTTGGCTTCTGCATGTACACAGCATCAGGAGTGCCTGG 420
Db 605 TTCTTGGCAATGTTACCCCTTTTGGCTTCTGCATGTACACAGCATCAGGAGTGCCTGG 664
Qy 421 ATCTCTGTGGGATCATATGATGCTTATCATGGCTTCTCAATAATGCTCCTGGACAGT 480
Db 665 ATCTCTGTGGGATCATATGATGCTTATCAUGCTTCTCAATAATGCTCCTGGACAGT 724
Qy 481 GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTTGCT 540
Db 725 GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTTGCT 784
Qy 541 AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCTGCCATTTTTCACA 600
Db 785 AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCTGCCATTTTTCACA 844
Qy 601 CTGAGCATCTGTTATCTGCTGATCATTTCCGGTTCTGTTAAAGTGGAGGTCCAGAAATCG 660
Db 845 CTGAGCATCTGTTATCTGCTGATCATTTCCGGTTCTGTTAAAGTGGAGGTCCAGAAATCG 904
Qy 661 GGCTCGGGGTTCTCACAGGAAGGCACTGACCAACCATCATCATCACCTTGATCATCTTC 720
Db 905 GGCTCGGGGTTCTCACAGGAAGGCACTGACCAACCATCATCATCACCTTGATCATCTTC 964
Qy 721 TTCTTGTGTTCTGCTCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAGTG 780
Db 965 TTCTTGTGTTCTGCTCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAGTG 1024
Qy 781 GGTATTATGAAAGACAGACTGCAATAAGCTTTTGGTTATCACACTGGCCCTTGGCAGCAGCC 840
Db 1025 GGTATTATGAAAGACAGACTGCAATAAGCTTTTGGTTATCACACTGGCTTGGCAGCAGCC 1084
Qy 841 AATGCTGCTTCAATCCTCTGCTCTATTAATTTGCTGGGAGAAATTTTAAGGACAGACTA 900
Db 1085 AATGCTGCTTCAATCCTCTGCTCTATTAATTTGCTGGGAGAAATTTTAAGGACAGACTA 1144
Qy 901 AAGCTGCACTCAGAAAGGCCATCACAGNAGGCAAGACAAAGTGTCTTCCCTGTT 960
Db 1145 AAGCTGCACTCAGAAAGGCCATCACAGNAGGCAAGACAAAGTGTCTTCCCTGTT 1204
Qy 961 AGTGTGTGTTGAGAAAGGAAACAGAGATATAA 993
Db 1205 AGTGTGTGTTGAGAAAGGAAACAGAGATATAA 1237
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RESULT 2

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US-09-044-404A-1
; Sequence 1, Application US/09044404A
; Patent No. 6200775
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: AMES, ROBERT
; APPLICANT: FOLEY, JAMES
; APPLICANT: SARAU, HENRY
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 790 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
```

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SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,404A
FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,795
FILING DATE: APRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH-70001-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-044-404A-1
Query Match 14.6%; Score 145.2; DB 3; Length 1578;
Best Local Similarity 51.5%; Pred. No. 1.1e-35;
Matches 451; Conservative 0; Mismatches 398; Indels 27; Gaps 4;
Qy 45 CACAATTGAAACTTCAAGAGAGAAATTTTCCCAATTTGTATATCTGATATAATATTTTCTG 104
Db 514 CACTATTGATGACTCCGCAATCAAGTGATTTCCACCTTGTACTCTATGATCTCTGTGT 573
Qy 105 GGGAGTCTTGGAAATGGTTGCTCATATATGTTTCTCGAGCCCTTATAAGAGTCCAC 164
Db 574 AGGCTCTTTGGCAATGGCTTTGTGCTCTATGTCTCTATAAAAAACCTATCAAGAAGTC 633
Qy 165 ATCTGTGAACGTTTTCATGCTAAATCTGGCAATTTCCAGATCTCCTGTTTCATAGCACGCT 224
Db 634 AGCCTTCCAGTATACATGATTAATTTAGCAGTAGCAGATCTACTTTGTGTGTGCACAT 693
Qy 225 TCCCTTCAGGGCTGACTATTTATCTTTAGAGGCTCCAAATGGATATTTGGAGACCTGGCCTG 284
Db 694 GCCTCTCCGTGGTCTATTATGTCACAAAGGCATTTGGCTCTTTGGTGACTTCTTGTG 753
Qy 285 CAGGATATGCTTATTCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTGACCGT 344
Db 754 CCGCCTCAGACCTATGCTTTGTATGTCAACCTCTATTGTAGCATCTTCTTTATGACAGC 813
Qy 345 GCTGAGTGTGTGGCTTTCTTGGCAATGGTTCCACCCCTTTCCGGCTTCTGCATGTCAACCAG 404
Db 814 CATGAGCTTTTCCGGTGCATTTGCAATTTTCCAGTCCAGAACATTAATTTGGTTAC 873
Qy 405 CATCAGGAGTGCCTGATCTCTGTGGGATCATATGGATTCCTT--ATCATGGCTTCCTC 461
Db 874 ACAGAAAAAAGCCAGGTTGTGTGTAGGTATTTGGATTTTGTGATTTTGACCAAGTTC 933
Qy 462 AATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCAATCATCTGTAGAGCT 521
Db 934 TCATTCTTAATGGCCAAACCAACCAAAAAGATGGGAAAAATAATACAAAGTCTTTGAGCC 993
Qy 522 GAATCTCTATAAAATTTGCTAAGCTGCA-----GACCATGAACATATATTGCCCTTGGTGT 575
Db 994 CCCACAAGACATCAAACTAAAAATCATGTTTTTGGTCTTGGCATTTATGTGTCATTGTTGT 1053
Qy 576 GGGCTGCTGCTGCCATTTTTCACACTCAGCATCTGTATCTGTGATCATTTCCGGGTTCT 635
Db 1054 TGGCTTTTATCATCCCTTTTGTATTATAATTTGTCTGTGTACACAATGATCATTTGACCTT 1113
Qy 636 GTTAAAGTGGAGGTCCAGAGATCGGGGTCTGGGTCTTCTCAGAGGAGGCACTGACCAAC 695
Db 1114 ACTAAAAAATCAATGAAAAAATAATCTGTCAAG-----TCATAAAAGGCTATAGGAAT 1167
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Qy 696 CATCATCATCACCTTGATCATCTTCTTCTTGTGTGTTCTGCTCCCTATCACACACTGAGGAC 755
Db 1168 GATCATGGTGTGACCGCTGCTCTTTTAGTCAGTTTCATGCAATATCATATTCACAGTAC 1227
Qy 756 CGTCCACTT-----GAGCATGGAAGTGGTTTATGCAAGACACTGCA 803
Db 1228 CATTCACCTTCATTTTATACAAATGAACCTTAAACCCCTGTGATCTGTCTTAAATGCA 1287
Qy 804 TAAAGCTTTGGTTATCACACTGGCTTGGCAGCAGCAATGCTGCTTCAATCCTCTGCT 863
Db 1288 GAAGTCGGTGTATACACTTGTCTCTGGCTGCATCCAAATGTTGCTTGGACCTCTCCT 1347
Qy 864 CTATTACTTTGCTGGGAGAAATTTAAGGACAGACT 899
Db 1348 ATATTCTTCTGGGGTAACTTTAGGAAAGGCT 1383

RESULT 3

US-09-586-924-1

; Sequence 1, Application US/09586924

; Patent No. 6506878

; GENERAL INFORMATION:

; APPLICANT: SATHE, GANESH M.

; APPLICANT: HALSEY, WENDY

; APPLICANT: ELLIS, CATHERINE E.

; APPLICANT: AMES, ROBERT S.

; APPLICANT: FOLEY, JAMES J.

; APPLICANT: SARAU, HENRY M.

; APPLICANT: CHAMBERS, JON

; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL

; TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR

; FILE REFERENCE: GH-70001-1D1

; CURRENT APPLICATION NUMBER: US/09/586,924

; PRIOR FILING DATE: 2000-06-05

; PRIOR FILING DATE: 1998-03-19

; PRIOR FILING DATE: 1997-04-22

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1578

; TYPE: DNA

; ORGANISM: HOMO SAPIENS

US-09-586-924-1

Query Match 14.6%; Score 145.2; DB 4; Length 1578;

Best Local Similarity 51.5%; Pred. No. 1.1e-35;

Matches 451; Conservative 0; Mismatches 398; Indels 27; Gaps 4;

Qy 45 CACAATTGMAAACTTCAAGAGAGAAATTTTCCCAATTGTATATCTGTATAATATTTTCTG 104
Db 514 CACTATTTGATGACTTCGCAATCAAGTGATTCACCTTGTACTCTATGATCTCTGTGT 573
Qy 105 GGGAGTCTTGGGAAATGGTGTGTCATATATGTTTTCTGAGCCTTATAGAAAGTCCAC 164
Db 574 AGGCTCTTTGGCAATGGCTTGTGCTCTATGTCTCATATAAAACCTATCACAGAAGTC 633
Qy 165 ATCTGTGAACGTTTTCAGTAAATCTGGCAATTCAGATCTCCTGTTTCATAGCAGCT 224
Db 634 AGCCTTCCAAGTATACATGATTAATTTAGCAGTAGCAGATCTACTTTGTGTGCACT 693
Qy 225 TCCCTTCAGGCTGACTATTATCTTAGAGGCTCAAATGGATATTTGGAGACCTTGGCTG 284
Db 694 GCCTCTCGGTGTCTATATATGTCACAAAGGCAATTTGGCTCTTTGGTGACTTCTTGTG 753
Qy 285 CAGGATATGCTTATTTCTTGTATGTCACACATGTACAGCAGTATTTATTTCTGACCGT 344
Db 754 CCGCTCAGCACCTATGCTTGTATGTCAACCTCTATTTAGCATCTCTTTATGACAGC 813
Qy 345 GCTGAGTGTGTGGTTTCTGGCAATGGTTTCACCCCTTTGGCTTCTGATGTCACAG 404
Db 814 CATGAGCTTTTCCGGTGCAATTGCAATGTTTTTCCAGTCCAGAACATTAATTTGGTTAC 873

Qy 405 CATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT---ATCATGGCTTCCCTC 461
Db 874 ACAGAAAAAGCCAGGTTTGTGTGTAGGTATTTGGATTTTGTGATTTTGGACAGTTC 933
Qy 462 AATAATGCTCTCGACAGTGGCTCTGAGCAGACGGCAGTGTACATCATGCTTTAGAGCT 521
Db 934 TCCATTTCTAATGGCCAAACCCACAAAAAGATGGGAAAAATAATACCAAGTGTCTTGAGCC 993
Qy 522 GAATCTCTATAAAATTGCTAAGCTGCA-----GACCATGAACCTATATTTGCTTTGGTGGT 575
Db 994 CCACAAGACAACTCAAACTTAAATCATGTTTTTGGTCTTGCATTTATGTGTCATTTGTTGT 1053
Qy 576 GGGCTGCTCTGCCAATTTTTCACACTCAGCATCTGTTATCTGCTGATCATTTCCGGTTCT 635
Db 1054 TGGCTTTATCATCCCTTTTGTATTATAAATGTTCTGTTACACAATGATCATTTTGGACCTT 1113
Qy 636 GTTAAAGTGGAGTCCCAGAAATCGGGCTGCGGTTTCTCACAGGAGGACACTGACCAC 695
Db 1114 ACTAAAAAAATCAATGAAAAAAATCTGTCAAG-----TCATAAAAAAGGCTATAGGAAT 1167
Qy 696 CATCATCATCACCTTGATCATCTTCTTGTGTGTTTCTGCCCTATCACACACTGAGGAC 755
Db 1168 GATCATGGTCTGACCGCTGCCCTTTTAGTCAGTTTCATGCCATATCATATTCAACGTAC 1227
Qy 756 CGTCCACTT-----GACGACATGGAAGTGGGTTTATGCAAGACAGACTGCA 803
Db 1228 CATTCACCTTCAITTTTTTACACAATGAACCTTAAACCCCTGTGATTTCTGCTTGAATGCA 1287
Qy 804 TAAAGCTTTGGTTATCACACTGSCCTTGGCAGCAGCAATGCCGTCTCAATCCTCTGCT 863
Db 1288 GAAGTCGGTGTTCATAACCTTGTCTCTGGCTGCATCCAATTTGTTGTTGACCCCTCTCCT 1347
Qy 864 CTATTACTTTGCTGGGAGAAATTTTAAAGACAGACT 899
Db 1348 ATATTCTTCTTCTGGGGTAACTTTAGGAAAAAGGCT 1383

RESULT 4

US-09-170-496D-31

; Sequence 31, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 1020

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-170-496D-31

Query Match 10.0%; Score 99.4; DB 4; Length 1020;
Best Local Similarity 48.8%; Pred. No. 4.1e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

Qy 71 TTTTCCCAATTGTATATCTGATAATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCA 130
Db 98 TGTTCGCTCTTCTACCTTCTGGATTTTATCTGGCTTTAGTTGGCAATACCTGGCTC 157
Qy 131 TATATGTTTTCTGACGCTTTATAAGAAAGTCCACATCTGTGAAGCTTTTCATGTAATC 190
Db 158 TGTGGCTTTTTCATCCGAGACCAAGTCCGGGACCCCGGCAACGTTCTCTGATGATC 217
Qy 191 TGCCCATTTGATCTCTCTGTTTCATAGCAGCTTCCCTTCAGGGCTGATTTATCTTA 250

Db 218 TGGCCGTGGCCGACTTGTGCTGGTGTGCTGCTGCCACCCGCCCTGGTCTACCACTTCT 277
; Sequence 1484, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US

Qy 251 GAGGCTCCATTTGGATATTTGGAGACTGGCTGCGAGGATATGCTTATTCCTTGTATG 310
Db 278 CTGGGAACCACTGGCCATTTGGGGAATCGCATGCCGTCTCACCGGCTTCTCTTACCC 337
Qy 311 TCAACATGTACACAGTATTTATTTCTGACCGTGTGAGTGTGTGGCGTTTCTCTGGCAA 370
Db 338 TCAACATGTACGACAGTATTTCTTCTGACCTGTGATGTGATGTGATGTGATGTGATGTG 397
Qy 371 TGGTTTCAACCTTTTCCGCTTCTGATGTGTACACAGCATCAGGAGTGTGCTGTGATCTCTGTG 430
Db 398 TTGTGACCGGTCAAGTCCCTCAAGCTCGCAGGCCCTCTACGACACACCTGGGCTGTG 457
Qy 431 GGATCATATGATCTTATCATGGCTTCTCAATATGCTTCTGGACAGTGGCTGTGAGC 490
Db 458 CCTTCTGTGGGTGGTGGTGTGGCCATGCGCCCTGCTGTGGTGGAGCCACAGACCG 517
Qy 491 AGAACGGCAGTGTACATCATGTCTTAGAGCTGAATCTCTATATAATTTGCTAAGCTGCAGA 550
Db 518 TGCAGACCAACACACAGTGGTCTGCTGAGCTGTACCGGGAAGGCTCCACCATG 577
Qy 551 CCATGAATATATGCTTGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
Db 578 CCTGG-----TGTCCCTGGCAGTGGCTTCACTTCCCGTTTCATCACCAGGTCACT 631
Qy 611 GTTATCTGCTGATCATTTCCGGTCTCTTAAAGTGGAGTCCAGAACTGGGGCTGGGG 670
Db 632 GCTACTGCTGATCATCCGAGCTCGGAGGCTCGGAGGCTGGGTGGAGAGCGCTCAAG- 690
Qy 671 TTCTTCAAGGAGGAGTGCACCATCATCATCATCATCATCATCATCATCATCATCATCAT 730
Db 691 -----ACCAAGGAGTGGCATGATCGCCATGATGCTGGCCATCTTCTGCTGTCT 742
Qy 731 TCTGCTCATCACACTGAGACCGTCCACTTG 765
Db 743 TGTGCTTACCACGTCAACCGCTCGGTCTAGCTG 777

RESULT 5

US-09-016-434-1484
; Sequence 1484, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1484:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g992699
; US-09-016-434-1484

Query Match 10.0%; Score 99.4; DB 4; Length 1900;

Best Local Similarity 48.8%; Pred. No. 6.1e-21;

Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

Qy 71 TTTTCCCAATTGTATATCTGATAATATTTTCTGGGAGTCTTGGGAAATGGTGTGCTCA 130
Db 797 TGTTCGCTCTCTTACCTTCTGGATTTATCTGGCTTTAGTTGGCAATACCTGGCTC 856
Qy 131 TATATGTTTTCTGAGCCTTATAAGAGTCCACATCTGTGAACGTTTTTCACTGCTAAATC 190
Db 857 TGTGGCTTTTCATCCGAGACCAAGTCCGGGACCCCGGCCAACGTTTCTGTGATGCATC 916
Qy 191 TGGCCATTTTCAGATCTCCCTGTTTATAAGACACGCTTCCCTTACGGGCTGACTATTCTTA 250
Db 917 TGGCGTGGCCACTTGTGCTGGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 976
Qy 251 GAGGCTCCAAATTTGGATATTTGGAGACCTGGCTGAGAGTATATGTTATTTCTTGTATG 310
Db 977 CTGGGAACCACTGGCCATTTGGGAAATCGCATGCCGTCTCACCGGCTTCTTCTTACC 1036
Qy 311 TCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGCTGCTTCTTCTGGCAA 370
Db 1037 TCAACATGTACGCCAGCATCTACTTCTCACCTGATGACGCCGACCGCTTCTGGCCA 1096
Qy 371 TGGTTTCAACCTTTCGGCTTCTGCATGTCCACAGCATCAGGAGTGCCTGGATCCTCTGTG 430
Db 1097 TTGTGACCCGCTCAAGTCCCTCAAGCTCCGAGGCCCTCTACGCACACCTGGCTGTG 1156
Qy 431 GGATCATATGATCTCTTATCATGGCTTCTCAATAATGCTCTGAGCAGTGGCTCTGAGC 490
Db 1157 CCTTCTGCTGGTGTGGTGGCTGTGGCCATGCGCCCGCTGCTGTGAGGCCACAGACCG 1216
Qy 491 AGAAGCGCAGTGTACATCATCTTGTAGCTGAATCTCTATAAATGTCTAAAGTGTGAGC 550
Db 1217 TGCAGACCAACCAACGCGTGTCTGCTGAGCTGTACCGGAGAGGCTTCCACCATG 1276
Qy 551 CCATGAACCTATATTCGCTTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
Db 1277 CCTGG-----TGTCCCTGGCAGTGGCTTCACTTCCGTTTCACTACACAGGTCACT 1330
Qy 611 GTTATCTGCTGATCATTCGGGTCTTGTATAAAGTGGAGTCCAGAAATCGGGGCTGCGGG 670
Db 1331 GCTACTGCTGATCATCCGAGCCTTGGGAGGCTGCTGCTGAGAGAGCGCTCAAG- 1389
Qy 671 TTTCTCAGGAAGGCACTGACCATCATCATCATCATCATCATCATCATCATCATCATCAT 730
Db 1390 -----ACCAAGGAGTGGCAGTGCATGATGCCCATGCTGCGCCATCTTCTTGGTCTGCT 1441
Qy 731 TCTGCGCTTATCACACACTGAGGACCGTCCACTTG 765
Db 1442 TGTGCGCTTACACGTCACCGCTCGGTCTAGCTG 1476

RESULT 6

US-08-153-848-43
; Sequence 43, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/153,848
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804e1, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 701..1717
US-08-153-848-43
Query Match 10.0%; Score 99.4; DB 1; Length 1901;
Best Local Similarity 48.8%; Pred. No. 6.1e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;
Qy 71 TTTTCCAAATGTATATCTGTATATATATTTTCTGGGAGTCTTGGGAATGGGTTGTCCA 130
Db 798 TGTTGGCTCTCTTACCTTCTGGATTTTATCTCTGGCTTTAGTTGGCAATACCTGGCTC 857
Qy 131 TATATGTTTCTCGACCTTATAGAAGTCCACATCTGTGAAGTTTTCATGCTAAATC 190
Db 858 TGTGGCTTTTTCATCCGAGACCAAGTCCGGGATCCCGGCAACAGTGTCTCTGATGATC 917
Qy 191 TGGCCATTTTCAGATCTCTGTGTATAGACAGCTTCTTCCCTTCAGGGCTGACTATTATCTTA 250
Db 918 TGGCCGTGGCGACTTGTGTGCTGTGTCTGTGCTTCCGCCACCGCTGGCTTCTTCT 977
Qy 251 GAGCTCCAATGTGATATTTGGAGACCTGGCTTCGAGGATATATCTTATTCCTTTGATG 310
Db 978 CTGGGAACCACTGGCCATTTGGGGAATCGATGCGCTCTCACGGCTTCTCTTCTTACC 1037
Qy 311 TCACATGTACAGCAGTATTTATTTCTGACCTGTGAGTGTGTGGTTTCTCTGGCAA 370
Db 1038 TCAACATGTACGCGAGCATCTACTTCTCTCATCTGATGAGGCGGACCGTTTCTGGCCA 1097
Qy 371 TGGTTTACCCCTTTGGCTTCTGATGTCCACGATCATCAGGAGTCCCTGGATCCTCTGTG 430
Db 1098 TTGTGACCCGGTCAAGTCCCTCAAGCTCCGACGGCCCTCTAGCACACCTGGCTGTG 1157
Qy 431 GGATCATATGATCCTTATCATGCTTCTCTCAATATATGCTCTCTGAGACAGTGGCTCTGAGC 490

Db 1158 CCTTCTGTGGGTGGTGGTGTGGCCATGCCCCCGCTGCTGGTGAGCCACAGACCG 1217
Qy 491 AGAACGSCAGTGTACATCATCTTAGAGCTGAATCTCTATAAAATTTGCTAAGCTGCAGA 550
Db 1218 TGCAGACCAACACACGGTGTCTGCTGAGCTGTACCGGGAGAGGCTTCCACCACATG 1277
Qy 551 CCATGAACATATATTTGCTTGGTGGGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
Db 1278 CCCTGG-----TGTCCCTGGCAGTGGCTTACCTTCCCGTTTCATCACCACGGTCACT 1331
Qy 611 GTTATCTGCTGATCATTCGGTCTGTAAAGTGGAGGTCCAGATCGGGGCTGGGG 670
Db 1332 GTTACCTGTGATCATCCGAGCTTGGCAGGCTGCGGAGGCTGCTGTGGAGAGCGCTCAAG- 1390
Qy 671 TTTCTCACAGGAAGGCACTGACCCACCATCATCATCATCATCATCTTCTTCTTCTTGTGTT 730
Db 1391 -----ACCAAGGCACTGCGCATGATGCCATGCTGCTGCTGCTGCTGCTGCTGCT 1442
Qy 731 TCTGCTTATCACACTGAGGACCGTCCACTTG 765
Db 1443 TCGTGGCTTACCACGTCACCGCTCGCTCTACGCTG 1477

RESULT 7

US-09-299-843A-43
Sequence 43, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/320598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single


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, FILING DATE: 06-JUNE-1995
, CLASSIFICATION:
, ATTORNEY/AGENT INFORMATION:
, NAME: MULLINS, J.G.
, REGISTRATION NUMBER: 30,073
, REFERENCE/DOCKET NUMBER: 325800-3666
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 201-994-1700
, TELEFAX: 201-994-1744
, INFORMATION FOR SEQ ID NO: 1:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 2453 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: DNA (genomic)
, FEATURE:
, NAME/KEY: CDS
, LOCATION: 548..1564
PCT-US95-07180-1

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Query Match	10.0%;	Score 99.4;	DB 5;	Length 2453;
Best Local Similarity	48.8%;	Pred. No. 7.2e-21;		
Matches 339;	Conservative 0;	Mismatches 341;	Indels 15;	Gaps 2;
Qy	71	TTTTTCCCAATTGTATATCTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTGCCA	130	
Db	645	TGTTTGGCTCTCTTCTACCTTCTGGATTTTATCTTGGCTTTAGTTGGCAATACCCCTGGGCTC	704	
Qy	131	TATATGTTTTCCTGCGACCTTATAAGAAAGTCCACATCTGTGAACGTTTTTCATGCTAAATC	190	
Db	705	TGTTGGCTTTTTCATCCGAGACACCAAGTCCGGGACCCCGCCCAAGCTTCTCTGATGCATC	764	
Qy	191	TGGGCATTTTCAGATCTCCTGTTTATAGACAGCTTCCCTTCAGGGCTGACTATTTATCTTA	250	
Db	765	TGGCCGTGGCGCACTTGTCTGCTGTGTGCTTCCCTGCCACCGGCTCTGCTTACCACCTCT	824	
Qy	251	GAGSCTCCAAATGGATATTTTGGAGACCTGGCCTGCAGGATTTATGTCTTATTTCCCTTGTATG	310	
Db	825	CTGGGAACCACTGGCCATTTTGGGGAATTCGATGCCGCTCTCACGGGCTTCTCTTCTTACC	884	
Qy	311	TCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGTTTTCTCTGGCAA	370	
Db	885	TCAACATGTACGCCAGCATCTACTTCTCACTGTCATCAGCGCCGACGGTTTCTCTGGCCA	944	
Qy	371	TGGTTTCACCCTTTCGGCTTCTGCATGTACAGCATCAGAGTGTGCTGATTCCTCTGTG	430	
Db	945	TTCTGCAACCCGGTCAAGTCCCTCAAGCTCCGCAAGGCCCTCTACGCACACCTGGGCTGTG	1004	
Qy	431	GGATCATATGGATCCCTTATCATGCTTCTTCAATAAATGCTCTGGACAGTGGCTCTGAGC	490	
Db	1005	CCTTTCTGTGGGTGGTGGTGGCTGTGGCCATGGCCCGCTGCTGTGGAGCCCAACAGACCG	1064	
Qy	491	AGAACGGCAGTGCACATCATGTCTTACGCTGAAATCTTATAAAATGCTAAAGCTGCAGA	550	
Db	1065	TGCAGACCACCAACGGTGGTCTGCCCTGCAGCTGTACCGGGAAGGCTCTCCACCATG	1124	
Qy	551	CCATGAACATATATGTCCTTGGTGGTGGGCTGCTGCTGCCATTTTTCACACTCAGCATCT	610	
Db	1125	CCCTGG-----TGTCCCTGGCATGGCCATTACCTTCCGGTTTCATCACCACGGTCACT	1178	
Qy	611	GTTTATCTGCTGATCATTTCCGGTTCTGTTAAAGTGGAGGTCCTCCAGATCCGGGCTGCGG	670	
Db	1179	GCTACTTGTCTGATCATCCCGAGCCTGGCGCAGGGCCTGCGGTGTGGAGAGCGCCCTCAAG	1237	
Qy	671	TTTTCTCAGGAAGGCACCTGACCACCATCATCATCTTGTATCATCTTCTTCTTGTGTT	730	
Db	1238	-----ACCAAGGCAGTGGCATGATGCCATAGTGTGGCCATCTTCTCTGTCTGCT	1289	
Qy	731	TCTTGCCTTATCACACTGAGACCGTGCACATTG	765	
Db	1290	TCTGTGCCCTACCAAGTCAACCGTCTCCCTTACGTG	1324	

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RESULT 11
US-09-170-496D-181
; Sequence 181, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous
; FILE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 181
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-181

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Query Match	9.7%	Score 96.2	DB 4	Length 1020
Best Local Similarity	48.5%	Pred. No. 4.4e-20		
Matches	337	Conservative 0	Mismatches 343	Indels 15
	Gaps 2			
Qy	71	TTTTCCCAATTGATATCTGATAATATTTTCTGGGGAGTCTTCGGGAAATGGGTTGTGCCA	130	
Db	98	TGTTGGCGCTCCCTTCTACCTCTCGGATTTTATCCTGGCTTTAGTTGGCAATAACCTCGGCTC	157	
Qy	131	TATATGTTTTTCCCTGCAGCCTTATAAGAAAGTCCACATCTGTGAACGTTTTTTCATGCTAAATC	190	
Db	158	TGTTGGCTTTTCATCCGAGACCAAGTCCGGGACCCCGGCCAACGTGTTCTTGATGCATC	217	
Qy	191	TGGGCATTTTCAGATCTCCTGTTCAATAGACAGCTTCCCTTCAGGGCTGACTATTTATCTTA	250	
Db	218	TGGCCGTGGCGCAGCTTGTCGTGGCTGTGCTCTGCCACCGGCTCGCTTACCACCTTCT	277	
Qy	251	GAGCTCCAATTCGATATTTTGGAGACCTGGCCTGCAGGATTTATGCTTTATTCCTTTGTATG	310	
Db	278	CTGGGAACCACTGGCCATTTTGGGAAATTCGATGCGCTCTACCGGCTTCCTCTTCTTACC	337	
Qy	311	TCAACATGTATACAGCAGTATTTATTTCTGACCGTGTCTGAGTGTGTGCGTTTTCTTGGCAA	370	
Db	338	TCAACATGTAGCCAGCATCTACTTCTCACTGTCATCAGGCGCGACGGTTTCTTGCCCA	397	
Qy	371	TGTTTACCCCTTTTGGCGTTCTGATGTCAACAGCATCAGAGGTGCTTGATTCCTCTGTG	430	
Db	398	TTGTGCAACCGGTCAGTCCCTCAAGCTCGCAGCGCCCTCTACGCACACCTTGGCCTGTG	457	
Qy	431	GGATCATATGATTCCTTATCATGGCTTCCCTCAATAATGCTCCTGGACAGTGGCTCTGAGC	490	
Db	458	CCTTCTGTGGGTGGTGGCTGTGGCCATGGCCCGCTGCTGGTGAGCCCAAGACCG	517	
Qy	491	AGAACGGCAGTGTACATCATGTCTAGAGCTGAATCTCTATAAATTTGCTTAAGCTGCAGA	550	
Db	518	TGCAGACCAACCACAGGTGGTGTGCTGTGAGCTGTACCGGGAGAGGCGCTCCCAACATG	577	
Qy	551	CCATGAACTATATTCCTTGGTGGTGGGCTGCCCTGCTGCCATTTTTTTCACACTCAGCATCT	610	
Db	578	CCCTGG-----TGTCCCTGGCAGTGCGCTTCACTTCCCGTTTCATCACACGGTCACT	631	
Qy	611	GTTATCTGCTGATCATTCGGGTTCTGTTAAAGTGGAGGTCCTCCAGATCGGGGCTGGGG	670	
Db	632	GCTACCTGTGTATCATCCGAGCGCTCGGAGGGGCTTGGGTGTGGAGAGCGCTCTCAAG-	690	
Qy	671	TTTCTCACAGGAAGGCACTGACCAACCATCATCATCACTTGAATCATCTTCTTCTGTGTT	730	
Db	691	-----ACCAAGGCAAAACGATGATCGCCATAGTGTGGCCATCTTCTGTGCTGCT	742	
Qy	731	TCCTGCGCTATCACACTGAGGACCGTCACTTG	765	
Db	743	TCGTGCGCTTACCAAGTCAACCGTCTGCTTACGTTG	777	

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Query Match	9.3%	Score 92;	DB 1;	Length 1255;
Best Local Similarity	54.4%;	Pred. No. 1.1e-18;		
Matches 185;	Conservative 0;	Mismatches 155;	Indels 0;	Gaps 0;
QY	49	ATTGAAACTTCAAGAGAGATTTTTCCCAATTGTATATCTGATAATATTTTCTGGGGA	108	
DB	266	ACTGGAAACCTGACCACCTGTCTTCCTTCCCAATTGTCTACAAATGTGTTGTGGTGGGT	325	
QY	109	GTCTTGGGAAATGGTTGTCCATATATGTTTTCTGCGAGCCTTATAAGAACTCCACATCT	168	
DB	326	TTGCCAAGTAACGGCATGGCCCTGTGGGTCTTTCTTTCCGAATAGAAAGACACCTT	385	
QY	169	GTGAACGCTTTTCATGCTAAATCTGGCCATTTTCAGATCTCTGTGTCATAAGCACGCTTCCC	228	
DB	386	GCTGTGATTTACATGGCCAACTCTGGCCTTGGCTGACCTCTCTCTGTCACTGTGTTCCCC	445	
QY	229	TTGAGGCTGACATTAATCTTAGAGGCTCCAAATTTGGATAATTTGAGACCTTGGCTCGAGG	288	
DB	446	TTGAAGATTTCCTATCATACATACATGGCAACAACTGGATTTATGGGAAGCTCTTTTGTAAAT	505	
QY	289	ATTATGCTTTATTCCTTGTATGTCAAATGTACAGCAGTATTTATTTCTTGACCGTGTCTG	348	
DB	506	GTGCTTATTGCGCTTTTTCATGGCAACATGTACTGTTCCTTTCTTCATGACCTGCCTC	565	

349 AGTGTGTCGTTCTCGCAATGTTTCACCCCTTTCGGC 388
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566 AGTGTGAGAGATTGGGTCATCGTGAACCCCATGGGGC 605
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RESULT 13
US-08-476-000-3
; Sequence 3, Application US/08476000
; Patent No. 5716789
; GENERAL INFORMATION:
; APPLICANT: SUNDELIN, JOHAN
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/390,301
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0006.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..1249
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 56
; US-08-476-000-3

Query Match	9.3%	Score 92	DB 1	Length 1255	
Best Local Similarity	54.4%	Pred. No. 1.1e-18			
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Db	266	ACTGGAACACTGACACTGCTCTCTCCCAATGTCTACAAATGTGTTGTGGTGGT	325		
Qy	109	GTCTTGGGAAATGGGTGTGCCATATATGTTTTCTCGAGCCTTATAAGAAGTCCACATCT	168		
Db	326	TTGCCAAGTAACGGCATGGCCCTGTGGGTCTTTCTTTCCGAACTAAGAAGACACCCCT	385		
Qy	169	GTGAACGTTTTATGCTAAATCTGGCCATTTACAGATCTCTGTTCATAAGCACGCTCCC	228		
Db	386	GCTGTGATTTACATAGGCCAAATCTGGCCCTTGGCTGACCTCTCTGTGCATCTGGTTCCCC	445		
Qy	229	TTCAGGCGTGACTATTATCTTTAGAGGCTCCAAATGGGATATTTGGAGACCTTGGCCTGCAGG	288		

Qy	49	ATTGAAACTTTCAAGAGAGAAATTTTCCCAATTGTATATCTGATAATATTTTCTGGGGA	108
Db	266	ACTGGAAACTGACCACCTGTCTTCCCTTCCAATTGTCTACACAAATTGTGTTGTGGTGGT	325
Qy	109	GTCTTGGGAAATGGTTGTCTCATATATGTTTCTCTGCAGCCTTATAAGAAGTCCACATCT	168
Db	326	TTGCCAAAGTAAACGGCATGGCCCTGTGGGTCTTTCTTTCCGAACCTAAGAAGAAGCACCCCT	385
Qy	169	GTGAACGTTTTCATGCTAAATCTGCCCAATTTTCAGATCTCCTGTTTCATAAGCACGCTTCCC	228
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Qy	349	AGTGTGTGCGTTTTCCTGGCAATGTTCCACCCCTTTTCGGC	388
Db	566	AGTGTGACAGGTATTGGGTCTCTGTGNAACCCCATGGGGC	605

Search completed: August 20, 2005, 07:35:01
Job time : 217 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2005, 04:38:00 ; Search time 3256 Seconds
(without alignments)

11608.667 Million cell updates/sec

Title: US-09-826-791A-1

Perfect score: 993

Sequence: 1 atggaaccaatggcacctt.....gaaaggaacaagagtataa 993

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: gb_est1.*
2: gb_est2.*
3: gb_hcc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	675	68.0	758	6	CD630086
3	666	67.1	762	6	CD630084
4	663	66.8	745	6	CD630072
5	661.2	66.6	726	6	CD630089
6	632	63.6	753	6	CD630075
7	619.2	62.4	750	6	CD630077
8	618	62.2	673	6	CD630069
9	607.2	61.1	729	7	CO959148
10	603	60.7	652	6	CD630079
11	599.4	60.4	670	6	CD630087
12	596.8	60.1	663	6	CD630081
13	593.4	59.8	629	6	CD630067
14	565	56.9	729	7	CF147785
15	543	54.7	633	6	CD630066
16	540.8	54.5	621	6	CD630074
17	539.6	54.3	1739	3	AK008997
18	521	52.5	844	6	CD630082
19	515.6	51.9	860	6	CD630070
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21	478.8	48.2	827	6	CD630073
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C 28	412	41.5	735	6	CD630085
C 29	404.6	40.7	812	6	CD630071
C 30	404.4	40.7	620	4	BI961697
31	339.2	34.2	605	4	BI960974
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C 33	301.2	30.3	319	8	AQ001459
C 34	179.4	18.1	604	1	A1178926
35	169.2	17.0	476	5	BX481095
C 36	146.8	14.8	996	3	CL092116
37	143.2	14.4	2755	3	AK033476
38	125	12.6	833	7	CO919341
39	123.4	12.4	842	7	CN503141
40	123.4	12.4	870	7	CO929273
41	121	12.2	720	7	CF147786
42	120.4	12.1	666	8	BZ214361
43	116.8	11.8	538	7	CV030948
44	116.4	11.7	671	6	CA376521
45	114	11.5	1352	3	CR667452

ALIGNMENTS

RESULT 1
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LOCUS CO959137 720 bp mRNA linear EST 17-AUG-2004
DEFINITION AGENCOURT 30842218 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389737 3', mRNA sequence.
ACCESSION CO959137
VERSION CO959137.1 GI:51323719
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 720)
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-x@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRB17 row: f column: 03
High quality sequence start: 20
High quality sequence stop: 632.
Location/Qualifiers
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/clone_lib="NIH_MGC_146"
/note="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file

ftp://image.llnl.gov.image.rearrayed_plates/IRBF_presv.dat
a. Note: this is a NIH_MGC Library."

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Db	720 GATTATGCTCTATTCCCTGTATGTCACATGTACAGCAGTATTATTCTCTGACCGTGCT	661	
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Db	660 GAGTGTGTGGGTTTCTCTGGCAATGGTTACCCCTTTCCGCTTCTGCATGTCCACGAGCAT	601	
QY	408 CAGGAGTCCCTGGATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCCTCAATAAT	467	
Db	600 CAGGAGTCCCTGGATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCCTCAATAAT	541	
QY	468 GCTCCTGACAGTGGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCTGAATCT	527	
Db	540 GCTCCTGACAGTGGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCTGAATCT	481	
QY	528 CTATAAAATTGCTAAGCTGCAGACCATGAATATATTGCTTGGTGGTGGCTGCCTGCT	587	
Db	480 CTATAAAATTGCTAAGCTGCAGACCATGAATATATTGCTTGGTGGTGGCTGCCTGCT	421	
QY	588 GCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCATTTCCGGTTCTGTAAAAAGTGA	647	
Db	420 GCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCATTTCCGGTTCTGTAAAAAGTGA	361	
QY	648 GGTCCAGAAATCGGGGCTCGGGTTTCTCACAGGAAGGCACTGACCACCATCATCATCAC	707	
Db	360 GGTCCAGAAATCGGGGCTCGGGTTTCTCACAGGAAGGCACTGACCACCATCATCATCAC	301	
QY	708 CTTGATCATCTTCTCTGTGTGTTTCTGCGCCTATCACACTGAGGACCGTCCACTTTGAC	767	
Db	300 CTTGATCATCTTCTCTGTGTGTTTCTGCGCCTATCACACTGAGGACCGTCCACTTTGAC	241	
QY	768 GACATGGAAAGTGGGTTTATGCAAGACAGACTGCAATAAGCTTTGGTTATCACACTGGC	827	
Db	240 GACATGGAAAGTGGGTTTATGCAAGACAGACTGCAATAAGCTTTGGTTATCACACTGGC	181	
QY	828 CTTGGCAGACCAATGCCTCTTCAATCCTCTGCTTATTTCTTGGTGGGAGAAATTT	887	
Db	180 CTTGGCAGACCAATGCCTCTTCAATCCTCTGCTTATTTCTTGGTGGGAGAAATTT	121	
QY	888 TAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAGGCAAAAGCAAGTG	947	
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QY	948 TGTTTTCCCTGTAGTGTGTGGTTGAGAAAAGGAAAAACAAGAGTATA	992	
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RESULT 2			
LOCUS	CD630086	758 bp	mRNA linear EST 12-JAN-2004
DEFINITION	56040032J1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD630086		
VERSION	CD630086.1	GI:40278352	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 758)		
TITLE	Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.		
JOURNAL	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes		
	Genomics 84 (1), 205-210 (2004)		

ORIGIN		Query Match 68.0%; Score 675; DB 6; Length 758; Best Local Similarity 98.9%; Pred. No. 5.4e-185; Matches 701; Conservative 0; Mismatches 5; Indels 3; Gaps 2;	
QY	1 ATGGAAACCAAAATGGCACTTCAGCAATAACAACAGCAGGAACCTGCACAATTTGAAAACTTC	60	
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Db	170 GGGTTGTCATATATGTTTTCTCGAGCCCTTATAGAAGTCCACATCTGTGAACGTTTTTC	229	
QY	181 ATGCTAAATCTGGCCATTTTCAGATCTCCTGTTTCAATAAGCAGCGTTCCCTTCAGGGCTGAC	240	
Db	230 ATGCTAAATCTGGCCATTTTCAGATCTCCTGTTTCAATAAGCAGCGTTCCCTTCAGGGCTGAC	289	
QY	241 TATTATCTTTAGAGGCTCCAAATTTGGATATTTTGAGACCTGGCTGCAAGGATATGTTCTTAT	300	
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QY	301 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTCTGACCGTGTGAGTGTGCGT	360	
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Db	650 ACTCAGCATCTGTTATCTGCTGATCATTCGCGGTTCTGTTAAAGTGGAGGTCCCAAGAATC	709	
QY	660 GGGGCTGCG--GGGTTTCTCACAGGAAGGCACATGACCACCATCATCATCA	706	
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LOCUS	CD630084		
DEFINITION	56040024J1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD630084		
VERSION	CD630084.1	GI:40278350	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 758)		
TITLE	Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.		
JOURNAL	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes		
	Genomics 84 (1), 205-210 (2004)		

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 762)
JOURNAL Circular rapid amplification of cDNA ends for high-throughput
COMMENT extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
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Best Local Similarity 99.4%; Pred. No. 2.3e-182;
Matches 700; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
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ACCESSION CD630072
VERSION CD630072.1 GI:40278338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 745)
JOURNAL Circular rapid amplification of cDNA ends for high-throughput
COMMENT extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
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Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 1.7e-181;
Matches 685; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
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QY 421 ATCTCTGTGGGATCATATGGATCTTATCATGGCTTCTCAATAATGCTTCTGGACAGT 480
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DB 530 GGGCTCTGAGCAGAACCGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTTGCT 589
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QY 541 AGCTGCAGACCATGACTATATTGCTTGGTGG-TGGGCTGCTGCTGCTGCTATTTTCAC 599
Db 590 AAGCTGCAGACCATGAACTATATTGCTTGGTGGCTGGGCTGCTGCTGCTATTTTCAC 649
QY 600 ACTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAA-AGTGGAGGTCACAGAAAT 658
Db 650 ACTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGTCCAGAAAT 709
QY 659 CGGGGCTGGGGTTTCTCAGAGAAAG 685
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RESULT 5
CD630089 726 bp mRNA linear EST 12-JAN-2004
LOCUS 56040096H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630089
ACCESSION CD630089
VERSION CD630089.1 GI:40278355
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 726)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
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ORIGIN
Query Match 56.6%; Score 661.2; DB 6; Length 726;
Best Local Similarity 99.4%; Pred. No. 5.6e-181;
Matches 674; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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QY 61 AAGAGAGAAATTTTCCCAATTGTATATCTGATAAATATTTTCTGGGAGTCTTGGGAAT 120
Db 110 AAGAGAGAAATTTTCCCAATTGTATATCTGATAAATATTTTCTGGGAGTCTTGGGAAT 169
QY 121 GGGTTGTCATATATGTTTTCTCGAGCCTTATAGAAGTCCACATCTCTGGAACGTTTTC 180
Db 170 GGGTTGTCATATATGTTTTCTCGAGCCTTATAGAAGTCCACATCTCTGGAACGTTTTC 229
QY 181 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCTATAAGCAGCGTTCCTTCAGGGGTGAC 240
Db 350 TCCCTGTATGTCAACATGTACAGCAGTATTTATTTCTCAGCGTGTGAGTGTGCGT 409
QY 361 TTCTCTGGCAATGGTTACACCCCTTTTCGGCTTCTGCAATGCCAGCATCAGGAGTGCCTGG 420

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Db 410 TTCCTGGCAATGGTTACCCCTTTTCGGCTTCTGCAATGTACAGCATCAGGAGTGCCTGG 459
QY 421 ATCTCTGTGGGATCATATGGATCCTTATCATGGCTTCTCTCAATAATGCTCCTGGACAGT 480
Db 470 ATCTCTGTGGGATCATATGGATCCTTATCATGGCTTCTCTCAATAATGCTCCTGGACAGT 529
QY 481 GGCTCTGACAGAACGGCAGTGTCAATCATGCTTTAGAGTGAATCTCTATAAAATTTGCT 540
Db 530 GGCTCTGACAGAACGGCAGTGTCAATCATGCTTTAGAGTGAATCTCTATAAAATTTGCT 589
QY 541 AAGCTGCAGACCATGAACATATATTGCTTGGTGGTGGCTGCTGCTGCCATTTTTCACA 600
Db 590 AAGCTGCAGACCATGAACATATATTGCTTGGTGGTGGCTG-CTGCTGCCATTTTTCACA 648
QY 601 CTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAAGTGAGGTCCAGAAATCG 660
Db 649 CTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAAGTGAGGTCCAGAAATCG 708
QY 661 GGGCTGGGGTTTCTCAC 678
Db 709 GGGCTGGGGTTTCTCAC 726

RESULT 6
CD630075 753 bp mRNA linear EST 12-JAN-2004
LOCUS 56039988H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630075
ACCESSION CD630075
VERSION CD630075.1 GI:40278341
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 753)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source
1..753
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 63.6%; Score 632; DB 6; Length 753;
Best Local Similarity 98.3%; Pred. No. 1.8e-172;
Matches 692; Conservative 0; Mismatches 5; Indels 7; Gaps 5;

QY 1 ATGGAAACCAATGGCACCTTCAGCAATAACAACAGCAGGAACCTGCACAATTGAAACCTTC 60
Db 50 ATGGAAACCAATGGCACCTTCAGCAATAACAACAGCAGGAACCTGCACAATTGAAACCTTC 109
QY 61 AAGAGAGAAATTTTCCCAATTGTATATCTGATAAATATTTTCTGGGAGTCTTGGGAAT 120
Db 110 AAGAGAGAAATTTTCCCAATTGTATATCTGATAAATATTTTCTGGGAGTCTTGGGAAT 169
QY 121 GGGTTGTCATATATGTTTTCTCGAGCCTTATAGAAGTCCACATCTCTGGAACGTTTTC 180
Db 170 GGGTTGTCATATATGTTTTCTCGAGCCTTATAGAAGTCCACATCTCTGGAACGTTTTC 229
QY 181 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCTATAAGCAGCGTTCCTTCAGGGGTGAC 240
Db 230 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCTATAAGCAGCGTTCCTTCAGGGGTGAC 289

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Qy 241 TATTATCTTAGAGCTCCAAATGGATATTTGGAGACCTGGCGCTCAGGATTTATGCTTAT 300
Db 290 TATTATCTTAGAGCTCCAAATGGATATTTGGAGACCTGGCGCTCAGGATTTATGCTTAT 349
Qy 301 TCCTTGATGTCACATGTACAGCAGTATTTATTTCTGACCGTCTGAGTGTGCGGT 360
Db 350 TCCTTGATGTCACATGTACAGCAGTATTTATTTCTGACCGTCTGAGTGTGCGGT 409
Qy 361 TTCTGCGCAATGGTTTACCCCTTTCCGCTTCTGATGTCACACGATCAGGAGTGCCTGG 420
Db 410 TTCTGCGCAATGGTTTACCCCTTTCCGCTTCTGATGTCACACGATCAGGAGTGCCTGG 469
Qy 421 ATCTCTGTGGGATCATATGGATCCTTATCATGCTTCTTCAATAATGCTCCTGGACAGT 480
Db 470 ATCTCTGTGGGATCATATGGATCCTTATCATGCTTCTTCAATAATGCTCCTGGACAGT 529
Qy 481 GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTA-TAAAAATGC 539
Db 530 GGCTCTGAGCAGAACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTA-TAAAAATGC 589
Qy 540 TAAGCTGACAGACCATGAATATTTGCTTGTGCTGGCTGCTGCTGCCA-TTTTTCA 598
Db 590 TAAGCTGACAGACCATGAATATTTGCTTGTGCTGGCTGCTGCTGCCA-TTTTTCA 649
Qy 599 CACTCAGCATCTGTTATCTG-CTGATCATTTGGGTTCTGTTTAAAGTGGAGTCCACGAA 657
Db 650 CACTCAGCATCTGTTATCTGCTGATCATTTGGGTTCTGTTTAAAGTGGAGTCCACGAA 708
Qy 658 TCGGGCTGCGGGTTTCTC-CACGAGGACATGACACCAT 698
Db 709 TCGGGCTGCGGGTTTCTC-CACGAGGACATGACACCAT 752

RESULT 7
CD630077 750 bp mRNA linear EST 12-JAN-2004
LOCUS 56039996H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630077
ACCESSION CD630077
VERSION CD630077.1 GI:40278343
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 750)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1. .750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

FEATURES
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Query Match 62.4%; Score 619.2; DB 6; Length 750;
Best Local Similarity 97.3%; Pred. No. 9.8e-169;
Matches 683; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

Qy 1 ATGGAACCAATGGCACCCTTCAGCAATAACAGCAGGAACTGCACAAATTTGAAACTTC 60
Db 50 ATGGAACCAATGGCACCCTTCAGCAATAACAGCAGGAACTGCACAAATTTGAAACTTC 109
Qy 61 AAGAGAGAAATTTTCCCAATTTGTATATCTGTATAATATTTTCTGGGGAGTCTTTGGGAAAT 120
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Db 110 AAGAGAGAAATTTTCCCAATTTGTATATCTGTATAATATTTTCTGGGAGTCTTTGGGAAAT 169
Qy 121 GGGTTGTCATATATGTTTCCCTGCAGCCTTATAAGAGTCCACATCTGTCAAGCTTTTC 180
Db 170 GGGTTGTCATATATGTTTCCCTGCAGCCTTATAAGAGTCCACATCTGTCAAGCTTTTC 229
Qy 181 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCAAGACGCTTTCCCTTCAGGGCTGAC 240
Db 230 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCAAGACGCTTTCCCTTCAGGGCTGAC 289
Qy 241 TATTATCTTAGAGCTCCAAATGGATATTTGGAGACCTGGCGCTCAGGATTTATGCTTAT 300
Db 290 TATTATCTTAGAGCTCCAAATGGATATTTGGAGACCTGGCGCTCAGGATTTATGCTTAT 349
Qy 301 TCCTTGATGTCACATGTACAGCAGTATTTATTTCTGACCGTCTGAGTGTGCGGT 360
Db 350 TCCTTGATGTCACATGTACAGCAGTATTTATTTCTGACCGTCTGAGTGTGCGGT 409
Qy 361 TTCTGCGCAATGGTTTACCCCTTTCCGCTTCTGATGTCACACGATCAGGAGTGCCTGG 420
Db 410 TTCTGCGCAATGGTTTACCCCTTTCCGCTTCTGATGTCACACGATCAGGAGTGCCTGG 469
Qy 421 ATCTCTGTGGGATCATATGGATCCTTATCATGCTTCTTCAATAATGCTCCTGGACAGT 480
Db 470 ATCTCTGTGGGATCATATGGATCCTTATCATGCTTCTTCAATAATGCTCCTGGACAGT 529
Qy 481 GGCTCTGAGCAGAACGGCAGTGTACACA-TCATGCTTAGAGCTGAATCTCTATAAAATGC 539
Db 530 GGCTCTGAGCAGAACGGCAGTGTACACATTCATGCTTAGAGCTGAATCTCTATAAAATGC 589
Qy 540 T-AAGCTGACAGACCATGAATATTTGCTTGTGCTGGGCTGCTGCTGCCATTTTTC 598
Db 590 TAAAGCTGCAGACCATGAATATTTGCTTGTGCTGGGCTG-CTGCTGCCATTTTTC 648
Qy 599 CACTCAGCATCTGTTATCTGCTGATCATTTGGGTTCTGTTTAA-AAGTGGAGTCCACGAA 657
Db 649 AACTCAGCATCTGTTATCTGCTGATCCTTCCGCTTCTGTTTAAACAGTGGAGTCCACGAA 708
Qy 658 TCGGGCTGCGGG--TTTCTCAGAGGAGGACCTGACACCA 697
Db 709 TCGGGCTGCGGGTTTCTCACCAGGAAGGACCTGAAACCA 750

RESULT 8
CD630069 673 bp mRNA linear EST 12-JAN-2004
LOCUS 56039916H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630069
ACCESSION CD630069
VERSION CD630069.1 GI:40278335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 673)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1. .673
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

FEATURES
source
ORIGIN
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Query Match      62.2%; Score 618; DB 6; Length 673;
Best Local Similarity 100.0%; Pred. No. 2.1e-168; Mismatches 0; Indels 0; Gaps 0;
Matches 618; Conservative 0;

QY 1 ATGGAACCAATGGCACTTCAGCAATAACAACAGCAGGAAGTGCACAAATGAAAACTTC 60
DB 50 ATGGAACCAATGGCACTTCAGCAATAACAACAGCAGGAAGTGCACAAATGAAAACTTC 109

QY 61 AGAGAGAGATTTTCCCAATTTGATATCTGATATATTTTCTGGGGAGTCTTGGAAAT 120
DB 110 AGAGAGAGATTTTCCCAATTTGATATCTGATATATTTTCTGGGGAGTCTTGGAAAT 169

QY 121 GGGTTCTGCATATATGTTTCTCGACGCTTATAAAGATCCACATCTGTGAACGTTTTC 180
DB 170 GGGTTCTGCATATATGTTTCTCGACGCTTATAAAGATCCACATCTGTGAACGTTTTC 229

QY 181 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCATAAGCAGCTTCCCTTCAGGGCTGAC 240
DB 230 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCATAAGCAGCTTCCCTTCAGGGCTGAC 289

QY 241 TATTATCTTAGAGGCTCCAAATTTGGATATTTGGAGACCTGGCCCTGCAGGATTAATGCTTAT 300
DB 290 TATTATCTTAGAGGCTCCAAATTTGGATATTTGGAGACCTGGCCCTGCAGGATTAATGCTTAT 349

QY 301 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTCGACCGTGTGAGTGTGTGCGT 360
DB 350 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTCGACCGTGTGAGTGTGTGCGT 409

QY 361 TTCCTGGCAATGGTTTCCACCCCTTTCGGCTTCTGCAATGTACACAGCATCAGGAGTGCCTGG 420
DB 410 TTCCTGGCAATGGTTTCCACCCCTTTCGGCTTCTGCAATGTACACAGCATCAGGAGTGCCTGG 469

QY 421 ATCTCTGTGGGATCATATGGATTCCTTATCATGGCTTCTCAATATATGCTCTGGACAGT 480
DB 470 ATCTCTGTGGGATCATATGGATTCCTTATCATGGCTTCTCAATATATGCTCTGGACAGT 529

QY 481 GGCTCTGACAGACGGCAGTGTACATCATGCTTAGAGTGAATCTCTATAAAATTTGCT 540
DB 530 GGCTCTGACAGACGGCAGTGTACATCATGCTTAGAGTGAATCTCTATAAAATTTGCT 589

QY 541 AAGCTGCAGACCATGAACATAATGCTTGGTGGTGGCTGCTGCTGCATATTTTTCACA 600
DB 590 AAGCTGCAGACCATGAACATAATGCTTGGTGGTGGCTGCTGCTGCATATTTTTCACA 649

QY 601 CTCAGCATCTGTATCTG 618
DB 650 CTCAGCATCTGTATCTG 667

RESULT 9
LOCUS CO959148
DEFINITION AGENCOURT_30842618 NIH_MGC_146 Homo sapiens cDNA clone IMAGE:7389737 5', mRNA sequence.
ACCESSION CO959148
VERSION CO959148.1 GI:51323730
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 729)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcapbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
CDNA Library Preparation: Guthrie cDNA Resource Center
```

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: IRBI7 row: f column: 03
High quality sequence stop: 602.

FEATURES
source

1..729
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7389737"
/tissue_type="mixed"
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/clone_lib="NIH_MGC_146"
/note="Vector: pcDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE Clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pcDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file ftp://image.llnl.gov/image.rearrayed_plates/IRBF.presv.dat
a. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 61.1%; Score 607.2; DB 7; Length 729;
Best Local Similarity 94.7%; Pred. No. 3e-165;
Matches 648; Conservative 0; Mismatches 32; Indels 4; Gaps 2;

QY 1 ATGGAACCAATGGCACTTCAGCAATAACAACAGCAGGAAGTGCACAAATGAAAACTTC 60
DB 50 ATGGAACCAATGGCACTTCAGCAATAACAACAGCAGGAAGTGCACAAATGAAAACTTC 109
QY 61 AGAGAGAGATTTTCCCAATTTGATATCTGATATATTTTCTGGGGAGTCTTGGAAAT 120
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QY 121 GGGTTCTGCATATATGTTTCTCGACGCTTATAAAGATCCACATCTGTGAACGTTTTC 180
DB 170 GGGTTCTGCATATATGTTTCTCGACGCTTATAAAGATCCACATCTGTGAACGTTTTC 229
QY 181 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCATAAGCAGCTTCCCTTCAGGGCTGAC 240
DB 230 ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCATAAGCAGCTTCCCTTCAGGGCTGAC 289
QY 241 TATTATCTTAGAGGCTCCAAATTTGGATATTTGGAGACCTGGCCCTGCAGGATTAATGCTTAT 300
DB 290 TATTATCTTAGAGGCTCCAAATTTGGATATTTGGAGACCTGGCCCTGCAGGATTAATGCTTAT 349
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DB 350 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTCGACCGTGTGAGTGTGTGCGT 409
QY 361 TTCCTGGCAATGGTTTCCACCCCTTTCGGCTTCTGCAATGTACACAGCATCAGGAGTGCCTGG 420
DB 410 TTCCTGGCAATGGTTTCCACCCCTTTCGGCTTCTGCAATGTACACAGCATCAGGAGTGCCTGG 469
QY 421 ATCTCTGTGGGATCATATGGATTCCTTATCATGGCTTCTCAATATATGCTCTGGACAGT 480
DB 470 ATCTCTGTGGGATCATATGGATTCCTTATCATGGCTTCTCAATATATGCTCTGGACAGT 529
QY 481 GGCTCTGACAGACGGCAGTGTACATCATGCTTAGAGTGAATCTCTATAAAATTTGCT 540
DB 530 GGCTCTGACAGACGGCAGTGTACATCATGCTTAGAGTGAATCTCTATAAAATTTGCT 589
QY 541 AAGCTGCAGACCATGAACATAATGCTTGGTGGTGGCTGCTGCTGCATATTTTTCACA 600
DB 590 AAGCTGCAGACCATGAACATAATGCTTGGTGGTGGCTGCTGCTGCATTTTTCACA 648
QY 601 CTCAGCATCTGTATCTGCTGATCATTTGGGTTCTGTTAAAGTGGAGAGTCCAGAGATCG 660

Db 649 CTCAGCATCTGTATCTGTCATCATCTCCGGTCTTTCTTAAATTTGAAG---TCNGAATC 705

Qy 661 GGCTCGGGGTTTCTACAGGAAG 684

Db 706 NNGCTCGGGGTTTTCACAAAGAAAG 729

RESULT 10

LOCUS CD630079 652 bp mRNA linear EST 12-JAN-2004

DEFINITION 5604008H1 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION CD630079

VERSION CD630079.1 GI:40278345

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 652)

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)

COMMENT Contact: Fu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com.

Location/Qualifiers

1. 652

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"

FEATURES

source

ORIGIN

Query Match 60.7%; Score 603; DB 6; Length 652;

Best Local Similarity 100.0%; Pred. No. 4.9e-164;

Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAACCAATGGCACCTTCAGCAATAACACAGCAGGAATGTCACAAATTTGAAACTTC 60

Db 50 ATGGAACCAATGGCACCTTCAGCAATAACACAGCAGGAATGTCACAAATTTGAAACTTC 109

Qy 61 AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTCTGGGAGTCTTGGGAAT 120

Db 110 AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTCTGGGAGTCTTGGGAAT 169

Qy 121 GGGTTGTCCATATATGTTTCTCGAGCTTTATAGAAGTCCACATCTGTGAACGTTTTC 180

Db 170 GGGTTGTCCATATATGTTTCTCGAGCTTTATAGAAGTCCACATCTGTGAACGTTTTC 229

Qy 181 ATGCTAAATCTGGCCATTTCAGATCTCTGTTTATAGAAGTCCACATCTGTGAACGTTTTC 240

Db 230 ATGCTAAATCTGGCCATTTCAGATCTCTGTTTATAGAAGTCCACATCTGTGAACGTTTTC 289

Qy 241 TATTATCTTAGAGCTCCAAATTTGATATTTGGAGACCTGGCCTGACGATTATGCTTTAT 300

Db 290 TATTATCTTAGAGCTCCAAATTTGATATTTGGAGACCTGGCCTGACGATTATGCTTTAT 349

Qy 301 TCCTTGTATGTCAACATGTACAGAGTATTTATTTCTGACCGTGTGAGTGTTCGCGT 360

Db 350 TCCTTGTATGTCAACATGTACAGAGTATTTATTTCTGACCGTGTGAGTGTTCGCGT 409

Qy 361 TTCTCGCAATGGTTTACCCCTTTCCGCTTCTGCAATGTACACAGCATCAGAGTGCCTGG 420

Db 410 TTCTCGCAATGGTTTACCCCTTTCCGCTTCTGCAATGTACACAGCATCAGAGTGCCTGG 469

Qy 421 ATCCTCTGTGGATCATATGATCCTTATCATGCTTCTCCTCAATATGCTCCTGGACAGT 480

Db 470 ATCCTCTGTGGATCATATGATCCTTATCATGCTTCTCCTCAATATGCTCCTGGACAGT 529

Qy 481 GGCTCTGAGCAGAACGGCAGTGTCAATCATATGCTTTAGAGCTGAATCTCTATAAAATTTGCT 540

Db 530 GGCTCTGAGCAGAACGGCAGTGTCAATCATATGCTTTAGAGCTGAATCTCTATAAAATTTGCT 589

Qy 541 AAGCTGCAGACCAATGAACCTATATTTGCTTGGTGGCTGCTGCTGCCATTTTTCACA 600

Db 590 AAGCTGCAGACCAATGAACCTATATTTGCTTGGTGGTGGCTGCTGCCATTTTTCACA 649

601 CTC 603

650 CTC 652

RESULT 11

LOCUS CD630087 670 bp mRNA linear EST 12-JAN-2004

DEFINITION 5604008H1 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION CD630087

VERSION CD630087.1 GI:40278353

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 670)

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)

COMMENT Contact: Fu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com.

Location/Qualifiers

1. 670

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"

FEATURES

source

ORIGIN

Query Match 60.4%; Score 599.4; DB 6; Length 670;

Best Local Similarity 99.7%; Pred. No. 5.5e-163;

Matches 611; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ATGGAACCAATGGCACCTTCAGCAATAACACAGCAGGAATGTCACAAATTTGAAACTTC 60

Db 50 ATGGAACCAATGGCACCTTCAGCAATAACACAGCAGGAATGTCACAAATTTGAAACTTC 109

Qy 61 AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTCTGGGAGTCTTGGGAAT 120

Db 110 AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTCTGGGAGTCTTGGGAAT 169

Qy 121 GGGTTGTCCATATATGTTTCTCGAGCTTTATAGAAGTCCACATCTGTGAACGTTTTC 180

Db 170 GGGTTGTCCATATATGTTTCTCGAGCTTTATAGAAGTCCACATCTGTGAACGTTTTC 229

Qy 181 ATGCTAAATCTGGCCATTTCAGATCTCTGTTTATAGAAGTCCACATCTGTGAACGTTTTC 240

Db 230 ATGCTAAATCTGGCCATTTCAGATCTCTGTTTATAGAAGTCCACATCTGTGAACGTTTTC 289

Qy 241 TATTATCTTAGAGCTCCAAATTTGATATTTGGAGACCTGGCCTGACGATTATGCTTTAT 300

Db 290 TATTATCTTAGAGCTCCAAATTTGATATTTGGAGACCTGGCCTGACGATTATGCTTTAT 349

Qy 301 TCCTTGTATGTCAACATGTACAGAGTATTTATTTCTGACCGTGTGAGTGTTCGCGT 360

Db 350 TCCTTGTATGTCAACATGTACAGAGTATTTATTTCTGACCGTGTGAGTGTTCGCGT 409

Qy 361 TTCTCGCAATGGTTTACCCCTTTCCGCTTCTGCAATGTACACAGCATCAGAGTGCCTGG 420


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Db      410 TTCTGGCAATGTTTACCCCTTTCCGCTTCTGCAATGTCACGAGCATCAGGAGTGCCTGG 469
Qy      421 ATCTCTGTGGGATCATATGGATCCCTATCATGCTTCTCATATAATGCTCCTGGACAGT 480
Db      470 ATCTCTGTGGGATCATATGGATCCCTATCATGCTTCTCATATAATGCTCCTGGACAGT 529
Qy      481 GGCTCTGAGCAGAACGGCAGTGTACATCATATGCTTTAGAGCTGAATCTCTATAAAATTGCT 540
Db      530 GGCTCTGAGCAGAACGGCAGTGTACATCATATGCTTTAGAGCTGAATCTCTATAAAATTGCT 589
Qy      541 AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCCATTTTTCACA 600
Db      590 AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCCATTTTTCACA 648
Qy      601 CTCAGCATCTGTT 613
Db      649 CTCAGCATCTGTT 661

RESULT 12
CD630081
LOCUS   CD630081
DEFINITION 56040016H1 FLP Homo sapiens cdNA, mRNA linear EST 12-JAN-2004
ACCESSION CD630081
VERSION   CD630081.1 GI:40278347
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 663)
AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE     Circular rapid amplification of cDNA ends for high-throughput
          extension cloning of partial genes
JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
          Incyte Genomics, Inc.
          3160 Porter Dr., Palo Alto, CA 94304, USA
          Tel: 6508454102
          Email: gfu@incyte.com.

FEATURES
source   Location/Qualifiers
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           /organism="Homo sapiens"
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ORIGIN
Query Match 60.1%; Score 596.8; DB 6; Length 663;
Best Local Similarity 99.3%; Pred. No. 3.2e-162;
Matches 610; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

Qy      1 ATGGAACCAAAATGGCACTTCAGCAATAACAACAGCAGGAAGTCACAAATTGAAAACCTTC 60
Db      50 ATGGAACCAAAATGGCACTTCAGCAATAACAACAGCAGGAAGTCACAAATTGAAAACCTTC 109
Qy      61 AAGAGAGAAATTTTCCCAATTTGATATCTGATATAATTTTCTGGGAGCTCTGGGAAT 120
Db      110 AAGAGAGAAATTTTCCCAATTTGATATCTGATATAATTTTCTGGGAGCTCTGGGAAT 169
Qy      121 GGCTTCTCCATATATGTTTCTTCGAGCCTTATAAGAAGTCACATCTGTGAACGTTTTC 180
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Qy      181 ATGCTAAATCTGGCCATTTTCAGATCTCCTGTTTATGAAGCAGCGTTCCCTTCAGGGCTGAC 240
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Qy      301 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTTCTGACCGTGCTGAGTGTGTGCGT 360
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Db      470 ATCTCTGTGGGATCATATGGATCCCTTATCATGCTTCTCATATAATGCTCCTGGACAGT 529
Qy      481 GGCTCTGAGCAGAACGGCAGTGTACATCATATGCTTTAGAGCTGAATCTCTATAAAATTGCT 540
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Qy      541 AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCCATTTTTCACA 598
Db      590 AAGCTGCAGACCAATGAACATATATGCTTGGTGGTGGCTGCTGCCATTTTTCACA 649
Qy      599 CACTCAGCATCTGTT 612
Db      650 CACTCAGCATCTGTT 663

RESULT 13
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LOCUS   CD630067
DEFINITION 56039908H1 FLP Homo sapiens cdNA, mRNA linear EST 12-JAN-2004
ACCESSION CD630067
VERSION   CD630067.1 GI:40278333
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE     Circular rapid amplification of cDNA ends for high-throughput
          extension cloning of partial genes
JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
          Incyte Genomics, Inc.
          3160 Porter Dr., Palo Alto, CA 94304, USA
          Tel: 6508454102
          Email: gfu@incyte.com.

FEATURES
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           /db_xref="taxon:9606"
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Best Local Similarity 97.2%; Pred. No. 3.1e-161;
Matches 615; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

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Db      110 AAGAGAGAAATTTTCCCAATTTGATATCTGATATAATTTTCTGGGAGCTCTTGGGAAT 169
Qy      121 GGCTTCTCCATATATGTTTCTTCGAGCCTTATAAGAAGTCACATCTGTGAACGTTTTC 180
Db      170 GGCTTCTCCATATATGTTTCTTCGAGCCTTATAAGAAGTCACATCTGTGAACGTTTTC 229
Qy      181 ATGCTAAATCTGGCCATTTTCAGATCTCCTGTTTATGAAGCAGCGTTCCCTTCAGGGCTGAC 240

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230	ATGCTAAATCTCGGCATTTTCAGATCTCTCTGTTCTATAAGACGCTTCCCTTCAGGGCTGAC	289
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290	TATTTATCTTAGAGGCTCCAAATTTGGGATATTTGGAGACCTGGCTCGCAGGATATATGTCCTTAT	349
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350	TCTCTGTATGTCACATGTACAGCAGTATTTATTTCTGACCGTGCTGAGTGTGTGCGGT	409
361	TTCTCTGGCAATGGTTTCAACCCCTTTTCGGCTTCTGCATGTCAACGACATCAGGAGTGCCTGG	420
410	TTCTCTGGCAATGGTTTCAACCCCTTTTCGGCTTCTGCATGTCAACGACATCAGGAGTGCCTGG	469
421	ATCTCTCTGTGGGATCATATGGGATCCTTATCANGCTTCCTCAATPAATGCTCTGGGACAGT	480
470	ATCTCTCTGTGGGATCATATGGGATCCTTATCANGCTTCCTCAATPAATGCTCTGGGACAGT	529
481	GGCTCTGACAGAAACGGGAGTGTCACATCATGCTTTAGAGCTGAATCTCTATAAAAA--TTG	538
530	GGCTCTGACAGAAACGGGAGTGTCACATCATGCTTTAGAGCTGAATCTCTATAAAAAATTGC	589
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599	CACCTAGCATCTGTTATCTGCTGATCATTTCCGG	631
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RESULT	14
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DEFINITION	AGENECONT 14740183 NIH MGC 145 Homo sapiens cDNA clone
	IMAGE:697I946 5', mRNA sequence.
ACCESSION	CFI147785
VERSION	CFI147785.1 GI:33244053
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 729)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S. Gerhard. Ph.D.

ORIGIN

Query Match	56.9%	Score 565	DB 7	Length 729
Best Local Similarity	100.0%	Pred. No. 6e-153		
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Qy	61	AAGAGAGAAATTTTCCCAATTTGTATATCTGATTAATATTTTTCTGGGAGAGCTTTGGGAAAT	120	
Db	225	AAGAGAGAAATTTTCCCAATTTGTATATCTGATTAATATTTTTCTGGGAGAGCTTTGGGAAAT	284	
Qy	121	GGGTTCTGCATATATGTTTTCTCGCGACCTTATAAGAAAGTCCACATCTGTGAACGTTTTC	180	
Db	285	GGGTTGTCCATATATGTTTTCTCGCGACCTTATAAGAAAGTCCACATCTGTGAACGTTTTC	344	
Qy	181	ATGCTAAATCTGGCCATATTCAGATCTCTCTGTTTATAGACAGCTTCCCTTCACGGGCTGAC	240	
Db	345	ATGCTAAATCTGGCCATATTCAGATCTCTCTGTTTATAGACAGCTTCCCTTCACGGGCTGAC	404	
Qy	241	TATTATCTTAGAGGCTCCAAATTGGATATTTGGAGACCTGGCGCTGCAGGATATATGTCATTAT	300	
Db	405	TATTATCTTAGAGGCTCCAAATTGGATATTTGGAGACCTGGCGCTGCAGGATATATGTCATTAT	464	
Qy	301	TCCTTGTATCTCAACATGTACAGCAGTATTTATTTCTTGACCGTGCTGAGTGTGTGCGGT	360	
Db	465	TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTTGACCGTGCTGAGTGTGTGCGGT	524	
Qy	361	TTCTCTGGCAATATGTTTCAACCCCTTTTCGGCTTCTGCATGTCAACGACATCAGAGAGTCCCTGG	420	
Db	525	TTCTCTGGCAATATGTTTCAACCCCTTTTCGGCTTCTGCATGTCAACGACATCAGAGAGTCCCTGG	584	
Qy	421	ATCCTCTGTGGGATCATATGGATCCCTTATCATGGCTTCCCTCAATAATGCTCCCTGGACAGT	480	
Db	585	ATCCTCTGTGGGATCATATGGATCCCTTATCATGGCTTCCCTCAATAATGCTCCCTGGACAGT	644	
Qy	481	GGCTCTGAGCAGAAACGGCAGTGTACATCATGCTTAGAGCTGGAATCTCTATAAAATTTGCT	540	
Db	645	GGCTCTGAGCAGAAACGGCAGTGTACATCATGCTTAGAGCTGGAATCTCTATAAAATTTGCT	704	
Qy	541	AAGCTGCAGACCATGAACATATATTG	565	
Db	705	AAGCTGCAGACCATGAACATATATTG	729	

RESULT 15

CD630066	CD630066	633 bp	linear	EST 12-JAN-2004
LOCUS	56039816K6	FLP Homo sapiens cDNA, mRNA sequence.		
DEFINITION	CD630066			
ACCESSION	CD630066.1	GI:40278332		
VERSION	EST.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1. (bases 1 to 633)			
AUTHORS	Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.			
TITLE	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes			
JOURNAL	Genomics 84 (1), 205-210 (2004)			
COMMENT	Contact: Fu GK Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102			

Email: gfu@incyte.com.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
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/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

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Best Local Similarity 99.8%; Pred. No. 1.5e-146;
Matches 554; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGGAAACCAATGGGACCTTCAGCAATTAACAACAGCAGGAACTGCACAATTGAAACTTC 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
50 ATGGAAACCAATGGGACCTTCAGCAATTAACAACAGCAGGAACTGCACAATTGAAACTTC 109
QY 61 AAGAGAGAATTTTCCCAATTGTATATCTGATAATATTTTCTGGGGAGTCTTTGGGAAAT 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
110 AAGAGAGAATTTTCCCAATTGTATATCTGATAATATTTTCTGGGGAGTCTTTGGGAAAT 169
QY 121 GGCTTCTCCATATATGTTTCTCGAGCCTTATAAGAACTCCACATCTCTGAAACGTTTTTC 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
170 GGCTTCTCCATATATGTTTCTCGAGCCTTATAAGAACTCCACATCTCTGAAACGTTTTTC 229
QY 181 ATGCTAAATCTGGCCATTTTCAGATCTCCTGTTTCAATAGCAGCCTTCCCTTCAGGGCTGAC 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
230 ATGCTAAATCTGGCCATTTTCAGATCTCCTGTTTCAATAGCAGCCTTCCCTTCAGGGCTGAC 289
QY 241 TATTATCTTAGAGGCTCCCAATTGGATATTTGGAGACTTGGCCTGCAGGATTAATGCTTAT 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
290 TATTATCTTAGAGGCTCCCAATTGGATATTTGGAGACTTGGCCTGCAGGATTAATGCTTAT 349
QY 301 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTCACCGTGTGAGTGTGTGCGT 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
350 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGT 409
QY 361 TTCTCTGGCAATGGTTCAACCTTTTCGGCTTCTGCATGTCAACGATCAGGAGTGCCTGG 420
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
410 TTCTCTGGCAATGGTTCAACCTTTTCGGCTTCTGCATGTCAACGATCAGGAGTGCCTGG 469
QY 421 ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCTCTCAATAATGCTCTGGACAGT 480
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
470 ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCTCTCAATAATGCTCTGGACAGT 529
QY 481 GGCTCTGAGCAGAAACGGCAGTGTACATCATGCTTAGAGC-TGAATCTCTATAAAATTGC 539
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
530 GGCTCTGAGCAGAAACGGCAGTGTACATCATGCTTAGAGCTTGAATCTCTATAAAATTGC 589
QY 540 TAAGCTGCAGACCAT 554
DB ||||||||||||||||
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Search completed: August 20, 2005, 07:31:15

Job time : 3259 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2005, 02:24:45 ; Search time 4426 Seconds
(without alignments)
10871.222 Million cell updates/sec

Title: US-09-826-791a-1
Perfect score: 993
Sequence: 1 atggaaccaaatggcaccctt.....gaaaggaacaagatataa 993

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_fa.*

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4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	993	100.0	993	6	AX304812 Sequence
2	993	100.0	993	6	BD131273 Novel pol
3	993	100.0	993	9	AB041644 Homo sapi
4	993	100.0	1026	6	AX644576 Sequence
5	993	100.0	1041	6	BD144304 Novel G-p
6	993	100.0	1041	6	CQ739544 Sequence
7	993	100.0	1041	6	AX148172 Sequence
8	993	100.0	1041	6	AX252467 Sequence
9	993	100.0	1041	6	AX281256 Sequence
10	993	100.0	1041	6	AX304816 Sequence
11	993	100.0	1041	6	AX417072 Sequence
12	993	100.0	1041	6	AX644551 Sequence
13	993	100.0	1041	6	BD131276 Novel pol
14	993	100.0	1041	9	AB083603 Homo sapi
15	993	100.0	1041	9	AF254664 Homo sapi
16	993	100.0	1041	9	AV389504 Homo sapi
17	993	100.0	1260	6	AX214087 Sequence
18	993	100.0	1260	6	AX214110 Sequence
19	993	100.0	1430	6	AX252469 Sequence

20	993	100.0	1430	6	AX281258 Sequence
21	993	100.0	1438	6	AX329226 Sequence
22	993	100.0	1625	6	AX319323 Sequence
23	993	100.0	1708	6	AX644523 Sequence
24	993	100.0	2549	9	BC069160 Homo sapi
25	993	100.0	2807	6	BD188750 Peptide 1
26	993	100.0	2807	6	AX549303 Sequence
27	993	100.0	2807	6	BD013097 Peptide 1
28	993	100.0	2807	9	AB038269 Homo sapi
29	993	100.0	2850	9	AF279611 Homo sapi
30	993	100.0	162446	9	AL137118 Human DNA
31	991	99.8	1039	6	AX211656 Sequence
32	989.8	99.7	1041	6	AX148246 Sequence
33	989.8	99.7	1401	6	AX349928 Sequence
34	989.8	99.7	1401	6	AX211539 Sequence
35	711.2	71.6	1038	4	AB052662 Sus scrofa
36	711.2	71.6	1101	6	BD188765 Peptide 1
37	711.2	71.6	1101	6	BD013112 Peptide 1
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39	622.6	62.7	1249	6	BD013115 Peptide 1
40	622.6	62.7	218951	2	AC111418 Rattus no
41	619.4	62.4	1385	10	AB058930 Mus muscu
42	614	61.8	170837	2	AC116884 Mus muscu
43	612.4	61.7	1762	10	AF331658 Rattus no
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45	192.4	19.4	284	10	AY462139 Chinchill

ALIGNMENTS

RESULT 1	AX304812	Sequence 1 from Patent EP1158050.	993 bp	DNA	linear	PAT 11-DEC-2001
LOCUS	AX304812					
DEFINITION	AX304812					
ACCESSION	AX304812.1	GI:17644492				
VERSION						
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REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						

ORIGIN

Query Match	100.0%;	Score 993;	DB 6;	Length 993;
Best Local Similarity	100.0%;	Pred. No. 2.9e-286;		
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Qy	61	AAGAGAGAATTTTCCCAATTTGATATCTGATATATTTTCTGGGAGCTTTGGGAAAT	120	
Dd	61	AAGAGAGAATTTTCCCAATTTGATATCTGATATATTTTCTGGGAGCTTTGGGAAAT	120	
Qy	121	GGTTGTTCATATATGTTTCTTCGAGCCCTTATAAGAGTCCACATCTGTGAACGTTTTC	180	
Dd	121	GGTTGTTCATATATGTTTCTTCGAGCCCTTATAAGAGTCCACATCTGTGAACGTTTTC	180	
Qy	181	ATCTAAATCTGGCCATTTTCAGATCTCTGTTTATAGACGCTTCCCTTCAGGGCTTGAC	240	
Dd	181	ATCTAAATCTGGCCATTTTCAGATCTCTGTTTATAGACGCTTCCCTTCAGGGCTTGAC	240	

QY	241	TATTATCTTAGAGCTCCAAATGGATATTTGGAGACCTGGCCCTGCAGGATTATGCTTAT	300
Db	241	TATTATCTTAGAGCTCCAAATGGATATTTGGAGACCTGGCCCTGCAGGATTATGCTTAT	300
QY	301	TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCCGTGCTGAGTGTGTGCGT	360
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QY	361	TTCTTGCAATGGTTACACCCCTTTCGCCCTTCTGCATGTCCAGAGATCAGGAGTGCCTGG	420
Db	361	TTCTTGCAATGGTTACACCCCTTTCGCCCTTCTGCATGTCCAGAGATCAGGAGTGCCTGG	420
QY	421	ATCCTCTGTGGGATCATATGATGCTTATCATGCTTCTCTCAATATGCTCCCTGGACAGT	480
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QY	481	GGCTCTGAGCAGAACGGCAGTGTACATCATGTCTTAGAGCTGAATCTCTATAAAATTTGCT	540
Db	481	GGCTCTGAGCAGAACGGCAGTGTACATCATGTCTTAGAGCTGAATCTCTATAAAATTTGCT	540
QY	541	AAGCTGAGACCAATGAATATATTTGGCTTGGTGGGCTGCTGCTGCCATTTTTCACA	600
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QY	601	CTCAGCATCTGTTATCTGCTGTATCATTTCCGGTTCTGTAAAGTGGAGTCCAGAAATCG	660
Db	601	CTCAGCATCTGTTATCTGCTGTATCATTTCCGGTTCTGTAAAGTGGAGTCCAGAAATCG	660
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Db	901	AAGTCTGCATCAGAAAGGCCATCCACAGAGGCAAGACAAAGTGTGTTTCCCTGTT	960
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LOCUS	BD131273	993 bp	DNA linear PAT 18-SEP-2002
DEFINITION	Novel polypeptide.		
ACCESSION	BD131273		
VERSION	BD131273.1	GI:23226218	
KEYWORDS	JP 2002017378-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Novel polypeptide		
JOURNAL	Patent: JP 2002017378-A 1 22-JAN-2002;		
COMMENT	PFIZER INC		
	OS Homo sapiens (human)		
	FN JP 2002017378-A/1		
	PD 22-JAN-2002		
PF	05-APR-2001	JP 2001106882	
PR	05-APR-2000	GB 0008504.3	
FI	HARLAND JEE		
PC	C12N15/09, A61K39/395, A61K39/395, A61K45/00, A61K48/00, A61P1/04,		
PC	A61P9/00,		
PC	A61P11/00, A61P11/02, A61P11/06, A61P19/00, A61P29/00, A61P31/00,		
PC	A61P37/00,		
PC	C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10	PC	
PC	C12N9/00, C12P21/02,		
PC	C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566,	PC	
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Best Local Similarity 100.0%; Pred. No. 2.9e-286;			
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGAAACCAATGGCCACTTCAGCAATAACAACAGCAGGAACCTGCACAATTTGAAAACTTC	60
Db	1	ATGGAAACCAATGGCCACTTCAGCAATAACAACAGCAGGAACCTGCACAATTTGAAAACTTC	60
QY	61	AAGAGAGAAATTTTCCCAATTTGTATATCTGATAATATTTTCTGGGGAGTCTTGGGAAAT	120
Db	61	AAGAGAGAAATTTTCCCAATTTGTATATCTGATAATATTTTCTGGGGAGTCTTGGGAAAT	120
QY	121	GGTTGTCTCATATATGTTTTCTCGACGCTTATAAGAGTCCACATCTCTGAAACGTTTTTC	180
Db	121	GGTTGTCTCATATATGTTTTCTCGACGCTTATAAGAGTCCACATCTCTGAAACGTTTTTC	180
QY	181	ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCATTAAGCAGCGTTCCTTCAGGGCTGAC	240
Db	181	ATGCTAAATCTGGCCATTTTCAGATCTCTGTTTCATTAAGCAGCGTTCCTTCAGGGCTGAC	240
QY	241	TATTATCTTAGAGCTCCAAATTTGGATATTTTGAGACCTGGCTGCAGGATTTATGCTTAT	300
Db	241	TATTATCTTAGAGCTCCAAATTTGGATATTTTGAGACCTGGCTGCAGGATTTATGCTTAT	300
QY	301	TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGT	360
Db	301	TCCTTGATGTCAACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGT	360
QY	361	TTCTTGGAATGGTTACCCCTTTTGGCTTCTGCATGTCCAGCAGATCAGGAGTGCCTGG	420
Db	361	TTCTTGGAATGGTTACCCCTTTTGGCTTCTGCATGTCCAGCAGATCAGGAGTGCCTGG	420
QY	421	ATCCTCTGGGATCATATGGAATCTTATCATGGCTTCTCAATATGCTCTCTGGACAGT	480
Db	421	ATCCTCTGGGATCATATGGAATCTTATCATGGCTTCTCAATATGCTCTCTGGACAGT	480
QY	481	GGCTCTGAGCAGAACGGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAAATTTGCT	540
Db	481	GGCTCTGAGCAGAACGGCAGTGTCAATCATGCTTAGAGCTGAATCTCTATAAAATTTGCT	540
QY	541	AAGCTGAGACCAATGAATATATTTGGCTTGGTGGGCTGCTGCTGCCATTTTTCACA	600
Db	541	AAGCTGAGACCAATGAATATATTTGGCTTGGTGGGCTGCTGCTGCCATTTTTCACA	600
QY	601	CTCAGCATCTGTTATCTGCTGTATCATTTCCGGTTCTGTAAAGTGGAGTCCAGAAATCG	660
Db	601	CTCAGCATCTGTTATCTGCTGTATCATTTCCGGTTCTGTAAAGTGGAGTCCAGAAATCG	660
QY	661	GGGCTCGGGTTTCTCACAGGAAGGCATGACACCATCATCATACCTTTGATCATCTTC	720

Qy	1	ATGGA	CCAAATG	GCACCTT	CAGCA	NATAA	CAACAG	CAGGA	ACTG	CA	CAATTTG	AAACCTTC	60				
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Qy	61	AAGAG	AGAAATTTT	CCCCAA	TGTAT	TATCTG	ATAAT	TAATTTT	CTGGG	AGTCT	CGGAAAT	120					
Db	109	AAGAG	AGAAATTTT	CCCCAA	TGTAT	TATCTG	ATAAT	TAATTTT	CTGGG	AGTCT	CGGAAAT	168					
Qy	121	GGGTTG	TCCATAT	ATATGTTT	TCTG	CAGCCTT	ATAAG	AAAGT	CCACAT	CTGTG	GAAGCTTTTC	180					
Db	169	GGGTTG	TCCATAT	ATATGTTT	TCTG	CAGCCTT	ATAAG	AAAGT	CCACAT	CTGTG	GAAGCTTTTC	228					
Qy	181	ATGCT	TAATCTG	GGCCATTT	CAGAT	CTCTG	TTTCA	TAA	GCACG	CTTCCCT	TCAGGCGTGAC	240					
Db	229	ATGCT	TAATCTG	GGCCATTT	CAGAT	CTCTG	TTTCA	TAA	GCACG	CTTCCCT	TCAGGCGTGAC	288					
Qy	241	TATTAT	CTTAG	AGGCTCCAA	TTGG	ATATTTG	GAGAC	CTGG	CGCTG	CAGGAT	TATGCTTTAT	300					
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Qy	301	TCCTTG	TATGT	CAACATG	TACAG	CAGTATTT	TATTT	CTG	ACCGT	GCTGAG	TGTGTGCGT	360					
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Qy	481	GGCT	CTG	AGCAG	AAGCG	CAGTGT	CACAT	CATGCTT	TAG	AGCTGA	ATCTCTATAAAATTGCT	540					
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Qy	541	AAGCT	G	CAG	ACCAT	GAAC	TATAT	TG	CCCTT	G	TG	TG	GGCTGCC	CTGTG	CCCATTTTTT	CACA	600
Db	589	AAGCT	G	CAG	ACCAT	GAAC	TATAT	TG	CCCTT	G	TG	TG	GGCTGCC	CTGTG	CCCATTTTTT	CACA	648
Qy	601	CTC	AGCAT	CTGTT	ATCTG	CTCAT	ATATG	CGGTT	CTGTT	AAAA	GGGAGGT	CCCCAGAA	TCG	660			
Db	649	CTC	AGCAT	CTGTT	ATCTG	CTCAT	ATATG	CGGTT	CTGTT	AAAA	GGGAGGT	CCCCAGAA	TCG	708			
Qy	661	GGGCT	G	GGGTTT	CTC	ACAG	GAAGG	CACTG	ACCA	CCATCAT	CTATC	ATCCTG	ATCAT	CTTC	720		
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Db	769	TTCTTG	TGTTT	CTG	CCCTAT	CAC	ACACT	GAGG	ACCGT	CCACTT	TGAC	GCACAT	TG	GAAGATG	828		
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Db	829	GGTTT	ATG	CA	AAAG	CAG	ACTG	CA	TAAAG	CTTTG	TTAT	CA	CACTG	GGCCTT	GGCAG	CGC	888
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Db	889	AAT	GCCTG	CTTCA	AT	CTCTG	CTAT	TAT	CTTCTG	CTGGG	AGAA	TTTTT	AAG	CA	CAG	ACTA	948
Qy	901	AAGT	CTG	CACTC	CAG	AAAA	AGG	CCATCC	ACAG	AAGG	CAAA	GACAA	AGATG	TGTTTT	CCCTG	TT	960
Db	949	AAGT	CTG	CACTC	CAG	AAAA	AGG	CCATCC	ACAG	AAGG	CAAA	GACAA	AGATG	TGTTTT	CCCTG	TT	1008
Qy	961	AGT	GTG	TG	TTG	A	GA	AAAG	GA	AAAC	AAAG	AGT	ATA	993			
Db	1009	AGT	GTG	TG	TTG	A	GA	AAAG	GA	AAAC	AAAG	AGT	ATA	1041			

RESULT 6
CQ739544
LOCUS CQ739544 1041 bp DNA
DEFINITION Sequence 25478 from Patent WO02068579.
linear PAT 03-FEB-2004

ACCESSION CQ739544
VERSION CQ739544.1 GI:42342834
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kix, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof

JOURNAL Patent: WO 02068579-A 25478 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES Location/Qualifiers
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Dh 709 GGGCTGGGGTTTCTCACAGGAAGGCACTGACCAACCATCATCATCACTTGATCATCTTC 768


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Db 949 AAGCTGCTCACTCAGAAAGGCCATCCACAGAGGCAAGCAAAAGTGTGTTTTCCCTGTT 1008
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Db 1009 AGTGTGTGTTGAGAAAGGAAACAAGAGTATAA 1041

RESULT 7
AX148172
LOCUS
DEFINITION
Sequence 13 from Patent WO0136471.
ACCESSION
AX148172
VERSION
AX148172.1 GI:14347079
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Chen,R., Dang,H.T. and Lowitz,K.P.
AUTHORS
Endogenous and non-endogenous versions of human g protein-coupled
TITLE
receptors
JOURNAL
Patent: WO 0136471-A 13 25-MAY-2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
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ORIGIN
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Query Match 100.0%; Score 993; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred.No.3e-286;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 169 GGGTTGTCATATATGTTTCTCGAGCCTTATAAGAACTGCACATCTGTGAACGTTTTTC 228
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Db 289 TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCCTGCAGGATTAATGCTTAT 348
QY 301 TCCTTGATGTCAACATGTACAGCAGTATTATTCTGACCGTGTGAGTGTGTGCGT 360
Db 349 TCCTTGATGTCAACATGTACAGCAGTATTATTCTGACCGTGTGAGTGTGTGCGT 408
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Db 1009 AGTGTGTGTTGAGAAAGGAAACAAGAGTATAA 1041

RESULT 8
AX252467
LOCUS
DEFINITION
Sequence 1 from Patent WO0168842.
ACCESSION
AX252467
VERSION
AX252467.1 GI:15985746
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Xiao,Y.
AUTHORS
Regulation of human p2y-like gpcr protein
TITLE
Patent: WO 0168842-A 1 20-SEP-2001;
JOURNAL
Bayer Aktiengesellschaft (DE)
FEATURES
Location/Qualifiers
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Query Match 100.0%; Score 993; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred.No.3e-286;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAACCAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAACTTC 60
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Db 49 ATGGAACCAATGGACCTTCAGCAATAACACAGCAGGAACCTGCACAAATTTGAAACTTC 108
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Db 169 GGGTGTGTCATATATGTTTCTCGACGCTTATAAGAAAGTCCACATCTGTGAAGCTTTTC 228
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Qy 961 AAGTGTGTTTGAAGAGGAAACAGAGATATA 993
Db 1009 AAGTGTGTTTGAAGAGGAAACAGAGATATA 1041

RESULT 9
AX281256
LOCUS AX281256 1041 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 1 from Patent WO0177149.
ACCESSION AX281256

VERSION AX281256.1 GI:16608512
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
- ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xiao, Y.
TITLE Regulation of human cyslt2-like gper protein
JOURNAL Patent: WO 0177149-A 1 18-OCT-2001;
Bayer Aktiengesellschaft (DE)
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Location/Qualifiers
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Query Match 100.0%; Score 993; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred. NO. 3e-286;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1009 AGTGTGCTGTGAGAAAGGAAACAAGAGTATAA 1041

RESULT 10
AX304816
LOCUS AX304816 1041 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 5 from Patent EP1158050.
ACCESSION AX304816
VERSION AX304816.1 GI:17644495
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Harland, L.
AUTHORS Human cysteinyl leukotriene receptor (cyslt2)
TITLE Patent: EP 1158050-A 5 28-NOV-2001;
JOURNAL Pfizer Limited (GB); PFIZER INC. (US)
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ORIGIN

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Query Match 100.0%; Score 993; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred. No. 3e-286;
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LOCUS AX417072 1041 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 6 from Patent WO0192302.
ACCESSION AX417072
VERSION AX417072.1 GI:21449674
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Murphy, P. and Martin, J.
AUTHORS Novel nucleic acids, polypeptides, methods of making, and uses
TITLE thereof
JOURNAL Patent: WO 0192302-A 6 06-DEC-2001;
FEATURES REGENERON PHARMACEUTICALS, INC. (US)
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Qy	121	GGGTGTGTCATATATGTTTCTCGACGCTTATAGAAGTCCACATCTGTGAACGTTTTC	180
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Qy	181	ATGCTAAATCTGGCCATTTCCAGATCTCTGTTTATAGACAGCGTTCCTCTTCAGGCGTGC	240
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Qy	1	ATGGAACCAATGGCACTTCAGCAATAACAACAGCAGGAACCTGCACAAATTTGAAAACCTTC	60
Db	49	ATGGAACCAATGGCACTTCAGCAATAACAACAGCAGGAACCTGCACAAATTTGAAAACCTTC	108
Qy	61	AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTTCTGGGAGCTCTGGGAAAT	120
Db	109	AAGAGAGAAATTTTCCCAATGTATATCTGATATATTTTCTGGGAGCTCTGGGAAAT	168
Qy	121	GGGTGTGTCATATATGTTTCTCGACGCTTATAGAAGTCCACATCTGTGAACGTTTTC	180
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Qy	181	ATGCTAAATCTGGCCATTTCCAGATCTCTGTTTATAGACAGCGTTCCTCTTCAGGCGTGC	240
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Qy	241	TATTATCTTAGAGCTCCAAATTTGGATATTTGGAGACCTGGCGCTTCAGGATATATGCTTTAT	300
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RESULT 13

BD131276
LOCUS Novel polypeptide.
DEFINITION Novel polypeptide.
ACCESSION BD131276
VERSION BD131276.1 GI:23226221
KEYWORDS JP 2002017378-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1041)
Lee,H.
Novel polypeptide
AUTHORS Patent: JP 2002017378-A 4 22-JAN-2002;
TITLE PFIZER INC
JOURNAL
COMMENT OS Homo sapiens (human)
PN JP 2002017378-A/4
PD 22-JAN-2002
PF 05-APR-2001 JP 2001106882
PR 05-APR-2000 GB 0008504.3

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Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 961 AGTGTGTGGTTGAGAAAGGAAACAAGAGTATAA 993
Db 1009 AGTGTGTGGTTGAGAAAGGAAACAAGAGTATAA 1041

RESULT 14
AB083603
LOCUS
DEFINITION
Homo sapiens GPCR gene for putative G-protein coupled receptor,
complete CDS, clone:hGPCR21.
ACCESSION
AB083603
VERSION
AB083603.1 GI:20152269
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Takeda S., Kadowaki S., Haga T., Takaesu H. and Mitaku S.
AUTHORS
TITLE
Identification of G protein-coupled receptor genes from the human
genome sequence
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1041)
Takeda S., Kadowaki S., Haga T., Takaesu H. and Mitaku S.
AUTHORS
TITLE
Direct Submission
JOURNAL
Submitted (10-APR-2002) Shigeki Takeda, Gunma University,
Department of Biological and Chemical, Engineering, Faculty of
Engineering; 1-5-1, Kiryu, Gunma 376-8515, Japan
(E-mail:stakeda@bce.gunma-u.ac.jp, Tel:+81-277-30-1434,
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ORIGIN

Query Match 100.0%; Score 993; DB 9; Length 1041;
Best Local Similarity 100.0%; Pred. No. 3e-286;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15

AP254664
LOCUS
DEFINITION
Homo sapiens cysteinyl leukotriene receptor CYSLT2 gene, complete

